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6612, Ap
5811, Ap
4204, Ap
6129, Ap
13197, A
3911, Ap
3600, Ap
30551, Ap
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8940, Ap
21724, A
489, App
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3, Appli
2, Appli
21, Appl
21, Appl
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                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                    (without alignments)
31.344 Million cell updates/sec
                                                        September 18, 2004, 04:20:54; Search time 9.88235 Seconds
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Sequence 4
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1: /cgn2_6/ptodata2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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-09-252-991A-21724
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-09-489-039A-13197
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US-09-252-991A-30551
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US-09-621-976-6612
US-09-621-976-5811
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US-10-009-999A-43
US-08-278-774-20
US-09-029-348-3
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US-08-963-825-21
US-09-500-811-21
US-09-570-573-21
US-09-548-608-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-500-811-15
US-09-570-573-15
US-09-548-608-15
                                                                                                                                                                      389414 segs, 51625971 residues
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                                                                                                                                                                                                                                                             Listing first 45 summaries
                                       - protein search, using sw model
                                                                                                                                                   Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                           Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                             Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                  US-10-615-959-39
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Match Length DB
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626
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                                                                                                                        Sequence:
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Sequence 3826, Ap	Sequence 4213, Ap	Sequence 3392, Ap	Sequence 74, Appl	Seguence 32, Appl	Sequence 9821, Ap	Sequence 6580, Ap	Sequence 6678, Ap	Seguence 18710, A	Sequence 8, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 8778, Ap	Sequence 28000, A	Sequence 13405, A	Sequence 10684, A
US-09-540-236-3826	US-09-134-000C-4213	US-09-540-236-3392	US-09-491-577-74	US-09-498-520A-32	US-09-489-039A-9821	US-09-134-000C-6580	US-09-134-000C-6678	US-09-252-991A-18710	US-07-637-870-8	US-07-637-399-5	US-08-112-703-5	US-08-559-260-2	US-08-901-547A-2	US-09-489-039A-8778	US-09-252-991A-28000	US-09-489-039A-13405	US-09-489-039A-10684
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319	355	356	363	376	426	426	426	438	440	440	440	444	444	449	454	463	479
84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4	84.4
27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27	27
28	29	30	31	32	33	34	35	98	37	38	39	40	41	4.2	43	44	45

## ALIGNMENTS

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APPLICANT: Eyre, David R.

APPLICANT: Eyre, David R.

TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS
FILLS REFERENCE: WGS-1-1-18220
CURRENT APPLICATION NUMBER: US/10/009,999A
CURRENT FILING DATE: 2003-01-22
PRIOR FILING DATE: 1999-12-10
PRIOR PLILING DATE: 1999-12-10
PRIOR PLILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 60/141,574
PRIOR APPLICATION NUMBER: US 60/141,574
PRIOR PLILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 60/142,675
PRIOR APPLICATION NUMBER: US 60/142,675
PRIOR PLILING DATE: 1999-07-02
PRIOR PLILING DATE: 1999-07-02
PRIOR PLILING DATE: 1999-08-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MISC_FEATURE
OTHER INFORMATION: synthetic peptide corresponding to carboxy-terminal
THEN INFORMATION: telopeptide sequence of human type III collagen
US-10-009-999A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                     Sequence 39, Application US/10009999A Patent No. 6602980 GENERAL INFORMATION:
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Patent No. 6110689
GENERAL INFORMATION:
APPLICANT: Qvist, Per
APPLICANT: Bonde, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Best Local Similarity
Matches 6; Conserv
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US-10-009-999A-39
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LENGTH: 6
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GENERAL INFORMATION:
APPLICANT: Ovist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·.
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                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/570,573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
CLONE: COLLAGEN TYPE III - ALPHA 1 - C TERM
                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GOGOTIS, Adda C.
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFRAX: 212-5237
                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Sequence 15, Application US/09570573
; Patent No. 6342361
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CLASSIFICATION :
PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
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STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MEDIUM TYPE: Floppy disk
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FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 236687
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
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OGY: linear
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Best Local Similarity
'''ng 6; Conserv?
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                A Method for Assaying Collagen Fragments in Body Fluids, A Teek Kit and Means for Carrying Out the Method and Use of the Method to Diagnose the Presence of Disorders Associated with the Metabolism of
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Patent No. 6323314

GENERAL INFORMATION:
APPLICANT: Ovist, Per
APPLICANT: Ovist, Per
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
TITLE OF INVENTION: Disorders Associated with the Metabolism of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
CORRESPONDENCES:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
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TITLE OF INVENTION: A Method for Assaying Collagen F TITLE OF INVENTION: in Body Fluids, A Test Kit and b TITLE OF INVENTION: in Body Fluids, A Test Kit and b TITLE OF INVENTION: in Body Fluids, A Test Kit and b TITLE OF INVENTION: Disorders Associated with the Me WOMBER OF SEQUENCES: 21
CORRESPONDENCES: 22
CORRESPONDENCES: 24
CORRESPONDENCES: 25
ADDRESSER: DATBY & DATBY PC
CITY: New York
STATE: New York
COUNTRY: USA
ZITE: 10022
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC Compatible
COMPUTER: PE PC-DOS/MS-DOS
CORPUTER: PETENTION NUMBER: US/OS/325
CURRENT APPLICATION DATA:
RELING DATE:
FILING DATE:
FIL
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) IMMEDIATE SOURCE:
) COLLAGEN TYPE III - ALPHA 1 - C TERM
US-08-963-825-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFCATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/187,319
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: GOGOTIE: Adda C
REGISTRATION NUMBER: 29,714
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEFAX: 212-527-7700
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FRAGMENT TYPE: C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 236687
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
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: USA
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TELEX: 2
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US-09-500-811-15
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MOLECULE TYPE: peptide
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
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                                                                                                                                                                                                                  Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 6; Conserv
  linear
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Best Local Similarity
Matches 6; Conserv
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US-10-009-999A-43
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TOPOLOGY:
                                                                                                                                 US-09-548-608-15
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Sequence 15, Application US/09548608

Barent No. 635542

GENERAL INFORMATION:
APPLICANT:
APPLICANT:
PAPLICANT:
BONde, Martin

TITLE OF INVENTION: A Method for Assaying Collagen Fragments

TITLE OF INVENTION: in Body Fluids, A Fest Kit and Means for Carrying Out the
TITLE OF INVENTION: Disorders Associated with the Metabolism of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
CORRESPONDENCE ADDRESS:
ADDRESSER: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
CCUTTY: New York
CCUTTY: New York
CCUTTY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/548,608
                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMEDIALIS SOURCE:
CLONE: COLLAGEN TYPE III - ALPHA 1 - C TERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEFRONE: 212-527-7700
TELEFAX: 212-753-6237
TELEFAX: 236697
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4305/08701
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT
NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REPERSONCHOCKET NUMBER: 4305,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 236687
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TENGTH: 7 amino acids
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Best Local Similarity 100.،
مومد 6; Conservative
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US-09-548-608-15
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APPLICANT: Eyre, David R.
APPLICANT: Eyre, David R.
FILLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS
FILLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS
FILLS OF INVENTION: SYNTHETIC DATE: 1999A
CURRENT FILLNG DATE: 1999-12-10
PRIOR PLICATION NUMBER: US/10/59/29357
PRIOR PLICATION NUMBER: US 60/141,574
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
PRIOR PLICATION NUMBER: US 60/142,274
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-07-02
PRIOR PLICATION NUMBER: US 60/142,675
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                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .,
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ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN TYPE III - ALPHA 1 - C TERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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Patent No. 6602980
GENERAL INFORMATION:
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Patent No. 6602980
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Query Match
Best Local Similarity 100...
5. Conservative
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5 EKAGGF 10
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Best Local Similarity
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US-08-963-825-21
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 3
LENGTH: 623
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                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MISC FEATURE OTHER INFORMATION: synthetic peptide corresponding to carboxy-terminal OTHER INFORMATION: telopeptide sequence of human type III collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/08278774

Patent No. 6653450
GENERAL INFORMATION:
APPLICANT: Berg, Richard A
APPLICANT: Toman, David P
APPLICANT: Toman, David P
APPLICANT: Wallace, Donald
ITILE OF INVENTION: MUTATED RECOMBINANT COLLAGENS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: COLLAGEN CORPORATION
STREET: 2500 Faber Place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,774
FILING DATE: 22-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RAFERORYO, KATHI L
REGISCOMMUNICATION INVERE: 36,644
RESTENDENCE/DOCKET NUMBER: 94-018
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (415) 354-4642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
PRIOR APPLICATION NUMBER: US 09/335,098
PRIOR FILING DATE: 1999-06-17
PRIOR PILING DATE: 1999-06-17
PRIOR PILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 60/141,574
PRIOR APPLICATION NUMBER: US 60/142,274
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PARENTIN VERSION 3.2
LENGTHARE: PARENTIN VERSION 3.2
LENGTH: 12
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Best Local Similarity 100...
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 2500 Faber
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: siz
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EKAGGF 12
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US-08-278-774-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 32; DB 3; Length 623; Best Local Similarity 100.0%; Pred. No. 94; Matches 6; Conservative 0; Mismatches 0; Indels
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100.0%; Score 32; DB 4; Length 15; 100.0%; Pred. No. 2.5;
                                                   0; Indels
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                                                                                                                                                                                                                                                  US-09-029-348-3
; Sequence 3, Application US/09029348
; Patent No. 6171827
; GENERAL INFORMATION:
; APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER
; TITLE OF INVENTION:
; CURRENT APPLICATION NOVEL PROCOLLAGENS
; CURRENT APPLICATION NUMBER: US/09/029,348
; CURRENT FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2. Application US/09029348

Patent No. 6171827

GENERAL INFORMATION:

APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER

TITLE OF INVENTION: NOVEL PROCOLLAGENS

FILE REFERENCE: 4087857PUS LISTING

CURRENT APPLICATION NUMBER: US/09/029,348

CURRENT APPLICATION NUMBER: 105/09/029,348

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 626
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0
                                                   0; Mismatches
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Gaps
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                                                                             COMPUTER: FLORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER:
COMPUTER: IBM PC COMPUTER:
COMPUTER: IBM PC COMPUTER:
APPLICATION NUMBER: US/09/500,811
FILING DATE:
APPLICATION NUMBER: 08/187,319
FILING DATE:
APPLICATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 212-527-7700
TELEPAX: 212-753-6237
TELEFAX: 21
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/570,573
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 805 Third Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity luv...
Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-500-811-21
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COUNTRY:
                                   COUNTRY:
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                      GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Ovist, Per
APPLICANT: Bonde, Martin

TITLE OF INVENTION: A Method for Assaying Collagen Fragments

TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the

TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of

TITLE OF INVENTION: Disorders Associated with the Metabolism of

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Darby & Darby PC

STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21, Application US/09500811
Patent No. 6323314
GENERAL INFORMATION:
APPLICANT: Gvist, Per
APPLICANT: Bonde, Martin
ITILE OF INVENTION: A Method for Assaying Collagen Fragments
ITILE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
ITILE OF INVENTION: Disorders Associated with the Metabolism of
CORRESPONDENCE ADDRESS:
ADDRESSEE: Boarby & Darby & Darby
STREEL: 805 Third Avenue
CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/187,319
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/963,825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (III)
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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Best Local Similarity
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STATE: New York
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Patent No. 6110689
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Sequence 21, Application US/09570573
Patent No. 6342361
GENERAL INFORMATION:
APPLICANT: Bonde, Martin
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out tTITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: ADDRESSE: Darby & Darby PC .. 0

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Search completed: September 18, 2004, 04:32:20 Job time : 10.8824 secs
               TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                              Query Match
Best Local Similarity 100...
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Best Local Similarity 83.3
Matches 5; Conservative
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US-09-252-991A-33096
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APPLICANT: Ovist, Per
APPLICANT: Ovist, Per
APPLICANT: Ovist, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: In Body Fluids, A Test Kit and Means for Carrying Out the
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
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                                                         NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFRAK: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4305/08701
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PARIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/09548608 Patent No. 6355442
APPLICATION NUMBER: 08/187,319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
COLLAGEN ALPHA 1 (III)
US-09-570-573-21
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NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
                                                                                                                                                            TELEFAX: 212-753-6237
TELERAX: 236687
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 236687
INPORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS: LENGTH: 1078 amino acids
                   FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
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US-09-548-608-21
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Sequence 33096, Application US/09252991A

Sequence 33096, Application US/09252991A

Sequence 33096, Application US/09252991A

Sequence 33096, Application US/09252991A

Sequence 33096, Application US CONTRIBLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

PIER REPREMENCE: 10999-02-18

CURRENT FILING DATE: 1999-02-18

PRIOR PILING DATE: 1999-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

SEQ ID NO 33096

LENGTH: 301

LENGTH: 301
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83.3%; Pred. No. 2.9e+02;
tive 0; Mismatches 1; Indels
amino acid
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September 18, 2004, 04:29:56; Search time 28.4706 Seconds (without alignments) 67.677 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		-39	-15	-41	-43	-11	US-09-864-408A-5882	US-10-767-701-33455	-19	78	US-10-437-963-162979	-21	-226	US-10-257-021-72	16.6	-33
ES		-959	-124	-959	-959	-125	-408	-701	-125	711-	-963	-124	-715	-021	-293	-822
SUMMARIES		JS-10-615-959-39	US-10-058-124-15	US-10-615-959-4	US-10-615-959-43	US-10-366-125-11	864	767	US-10-366-125-19	JS-09-908-711-78	437	058	918	257	177	US-10-301-822-33
SUM		-10	-10	-10-	-10	-10.	-60-	-10	-10-	9-60	-10	-10-	-00	-10-	-10-	-10
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-10-402-089- -10-402-089- -10-402-089-	US-10-402-0/ZA-6 US-10-402-0/ZA-12 US-10-357-851-3 US-10-358-024-3 US-10-734-564-103	10-094-679-3 10-437-963-15 10-425-114-46 10-437-963-13	-10-437-963-2 -10-437-963-1 -10-425-114-5	-10-425-114-3 -10-1455-114-3 -10-424-599-2 -10-408-765A-	925-301-142 -408-765A-4 -935-642-10 -221-278-22 -170-385-25 -316-253-30	172-22
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### ALIGNMENTS

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** APPLICANT: Byte, David R.

** APPLICANT: Byte, David R.

** TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS

** FILE REPERENCE: WROS-1-18220

** CURRENT APPLICATION NUMBER: US/10/615,959

** CURRENT APPLICATION NUMBER: US/10/009,999A

** PRIOR APPLICATION NUMBER: Byt/US99/29357

** PRIOR PILING DATE: 1099-12-10

** PRIOR PILING DATE: 1999-12-10

** PRIOR FILING DATE: 1999-12-10

** PRIOR FILING DATE: 1999-06-17

** PRIOR PILING DATE: 1999-06-17

** PRIOR PILING DATE: 1999-06-17

** PRIOR PILING DATE: 1999-07-02

** PRIOR PILING DATE: 1999-07-07

** PRIOR PILING DATE: 1999-08-30

** NUMBER OF SEQ ID NOS: 45

** SEQ ID NOS: 45

** LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: MISC FEATURE
OTHER INFORMATION: synthetic peptide corresponding to carboxy-terminal
OTHER INFORMATION: telopeptide sequence of human type III collagen
US-10-615-959-39
                            Sequence 39, Application US/10615959
Publication No. US20040048321A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
US-10-615-959-39
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100.0%; Score 32; DB 12; Length 6; 100.0%; Pred. No. 1.2e+06; Query Match Best Local Similarity

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SEGURATION NO. US20040048321A1

GENERAL INFORMATION:

APPLICATION NO. US20040048321A1

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/009,999A

PRIOR FILING DATE: 2003-07-08

CURRENT PELICATION NUMBER: US/10/009,999A

PRIOR FILING DATE: 2003-01-02

PRIOR FILING DATE: 1999-12-10

PRIOR PELICATION NUMBER: US 09/335,098

PRIOR PELICATION NUMBER: US 60/141,574

PRIOR FILING DATE: 1999-06-17

PRIOR PELICATION NUMBER: US 60/142,274

PRIOR FILING DATE: 1999-07-02

PRIOR FILING DATE: 1999-07-02

PRIOR FILING DATE: 1999-07-03

PRIOR FILING DATE: 1999-07-03

PRIOR FILING DATE: 1999-08-30

PRIOR FILING DATE: 1999-08-30

PRIOR FILING DATE: 1999-08-30

NUMBER OF SEQ ID NOS: 45

SEQ ID NOS: 45

SEQ ID NOS: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MISC FEATURE OTHER INFORMATION: Synthetic peptide corresponding to carboxy-terminal OTHER INFORMATION: telopeptide sequence of human type III collagen
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100.0%; Pred. No. 1.2e+06;
tive 0; Mismatches 0;
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; Publication No. US20040048321A1
; GENERAL INFORMATION:
Sequence 41, Application US/10615959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin version 3.2 SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity luv...
5, Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: A Method for Assaying Collagen Fragments in Body Fulids, A Test Kit and Means for Carrying Out the Method and Use of the Method to Diagnose the Presence of Disorders Associated with the Metabolism of
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MEDIUM TYPE: FORM;

COMPUTER: IBM PC compatible

COMPUTER: IBM PC Compatible

COMPUTER: Batentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/058,124

FILING DATE: 29-Jan-2002

CLASSIFICATION NUMBER: 09/570,573

FILING DATE: 2002-MAY-12

APPLICATION NUMBER: 08/187,319

FILING DATE: CUNCHOWN>

ATTORNEY/AGDAT INFORMATION:

NAME: GGGOTIS, Adda C

REGISTRATION NUMBER: 29,714

REFERENCE/DOCKET NUMBER: 4305/08701

TELEPHONE: 212-52-7700

TELEPHONE: 212-73-6237

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 32; DB 14; Length 7; Best Local Similarity 100.0%; Pred. No. 1.2e+06; Matches 6; Conservative 0; Mismatches 0; Indels
          Indels
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          ö
          Mismatches
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
                                                                                                                                          RESULT 2
US-10-058-124-15
i Sequence 15, Application US/10058124
j Publication No. US20030119058A1
j GENERAL INFORMATION:
APPLICANT: Qvist, Per
APPLICANT: Application Martin
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MOLECULE TYPE: peptide
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
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            6; Conservative
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ZIP: 10022
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US-10-615-959-41
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Sequence 33455, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kovi, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NOS: 63128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hellerstein, Marc
TITLE OF INVENTION: MEASUREMENT OF BIOSYNTHESIS AND BREAKDOWN RATES OF
TITLE OF INVENTION: BIOLOGICAL MOLECULES THAT ARE INACCESSIBLE OR NOT
TITLE OF INVENTION: BIOLOGICAL MOLECULES THAT ARE INACCESSIBLE OR NOT
TITLE OF INVENTION: BY LABEL INCORPORATION INTO METABOLIC DERIVATIVES AND
TITLE OF INVENTION: CATABOLITIC PRODUCTS
TITLE OF INVENTION: CATABOLITIC PRODUCTS
TITLE OF INVENTION NUMBER: US/10/366,125
CURRENT APPLICATION NUMBER: US/06/125
CURRENT FILING DATE: 2003-02-12
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C32355_1.pep
US-10-767-701-33455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-366-125-19
; Sequence 19, Application US/10366125
; Publication No. US20030228259A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
                                                            EKAGGF 33
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US-09-908-711-78
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| Sequence 5882, Application US/09864408A
| Sequence 5882, Application US/09864408A
| Publication No. US20040009474A1
| GENERAL INFORMATION:
| APPLICANT: Shinkets, Richard A. | APPLICANT: Shinkets, Richard A. | TITLE OF INVENTION: No. US20040009474A1el Human Polynucleotides and Polypeptides Encor FILE REFERENCE: 21402-012
| CURRENT APPLICATION NUMBER: US/09/864,408A | CURRENT FILING DATE: 2001-05-24
| PRIOR APPLICATION NUMBER: 602206,690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hellerstein, Marc

APPLICANT: Hellerstein, Marc

ITILE OF INVENTION: MEASUREMENT OF BIOSYNTHESIS AND BREAKDOWN RATES OF

ITILE OF INVENTION: BIOLOGICAL MOLECULES THAT ARE INACCESSIBLE OR NOT-

ITILE OF INVENTION: EASILY ACCESSIBLE TO DIRECT SAMPLING, NON-INVASIUELY,

ITILE OF INVENTION: BY LABEL INCORPORATION INTO METABOLIC DERIVATIVES AND

ITILE OF INVENTION: CATABOLITIC PRODUCTS

FILE REFERENCE: 416272003500

CURRENT APPLICATION NUMBER: US/10/366,125

PRIOR APPLICATION NUMBER: US/6/326,008

PRIOR PRING DATE: 2002-02-12

PRIOR PLING DATE: 2002-02-12

NUMBER OF SEQ ID NOS: 28

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11

ITVPE: PRI

TYPE: PRI

VOCANIESH: Home sapiens
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FBATURE:
NAME/KEY: MISC_FEATURE
OTHER INFORMATION: synthetic peptide corresponding to carboxy-terminal
OTHER INFORMATION: telopeptide sequence of human type III collagen
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0
                                                                                                                                                          Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 32; DB 15; Length 25; 100.0%; Pred. No. 16; cive 0; Mismatches 0; Indels
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                                                                                                                                                  100.0%; Score 32; DB 12; I
100.0%; Pred. No. 7.5;
tive 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5882
LENGTH: 51
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/1036125
Publication No. US20030228259A1
GENERAL INFORMATION:
                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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; ORGANISM: Homo sapiens
US-09-864-408A-5882
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                                                                                                      US-10-615-959-43
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GENERAL INTERCANTION: Nucleic Acids, Proteins, and Antibodies TITLE OF INVESTION: Nucleic Acids, Proteins, and Antibodies FILLE REPRESENCE: PALSE CURRENT PARELICATION NUMBER: 1051/01560 PRIOR PLILING DATE: 2001-01-746, 867 PRIOR PLILING DATE: 2001-01-74 PRIOR APPLICATION NUMBER: 1091/64, 892 PRIOR PLILING DATE: 2001-01-17 PRIOR PLILING DATE: 2001-01-17 PRIOR PRILICATION NUMBER: 1091/64, 991 PRIOR PLILING DATE: 2001-01-17 PRIOR APPLICATION NUMBER: 1091/64, 991 PRIOR PLILING DATE: 2001-01-17 PRIOR PRILICATION NUMBER: 1091/64, 991 PRIOR PRILICAT
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Shou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, B
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NAME/KEY: SITE
LOCATION: (2)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (4)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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US-10-058-124-21
; Sequence 21, Application US/10058124
; Publication No. US20030119058A1
; GENERAL INFORMATION:
; APPLICANT: Qvist, Per
; APPLICANT: Qvist, Per
; APPLICANT: Qvist, Martin
; TITLE OF INVENTION: A Method for Assaying Collagen Fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 32; DB 9; Length 309; 100.0%; Pred. No. 1.9e+02; rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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100.0%; Pred. No. 3e+02;
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; Publication No. US20040123343A1
; GENERAL INFORMATION:
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180, 628
PRIOR PILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/209,467
PRIOR FILING DATE: 2000-06-07
NUMBER: OF SEQ ID NOS: 167
SOFTWARE: PATENTIN Ver. 2.0
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Best Local Similarity 100..
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Best Local Similarity 100.
"Lag 6; Conservative
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ORGANISM: Oryza sativa
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US-10-437-963-162979
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TYPE: PRT
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Similarity 100.0%; Score 32; DB 12; Length 1466;
Similarity 100.0%; Pred. No. 9e+02;
6; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                               Query Match
100.0%; Score 32; DB 12; Length 1
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Morin, Patrice J.
APPLICANT: Sherman-Baust, Cheryl A.
APPLICANT: Sherman-Baust, Cheryl A.
APPLICANT: Pizer, Bllen S.
APPLICANT: Hough, Colleen D.
TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER FILE REFERENCE: 14014.0369U2
CURRENT PELICATION NUMBER: US110/257,021
CURRENT PILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: PCT/US01/10947
PRIOR PILING DATE: 2001-04-03
PRIOR PILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PSELEED for Windows Version 4.0
         NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 226
LENGTH: 1466
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 72, Application US/10257021
Publication No. US20030211498A1
GENERAL INFORMATION:
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Publication No. US20030124128A1
GENERAL INFORMATION:
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Hortobagyi, Gabriel N.
Pusztai, Lajos
Meric, Funda
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Hoersch, Sebastian
Monahan, John
Meyers, Rachel E.
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Kamatkar, Shubhangi
Mertens, Maureen
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Wang, Youzhen
                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
US-09-918-715-226
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APPLICANT: Glatt, Karen
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; ORGANISM: Homo sapiens
US-10-257-021-72
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Best Local Similarity
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US-10-177-293-68
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APPLICANT:
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in Body Fluids, A Test Kit and Means for Carrying Out the Method and Use of the Method to Diagnose the Presence of Disorders Associated with the Metabolism of
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                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPANING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/058,124
FILING DATE: 29-Jan-2002
CLASSIFICATION NUMBER: 09/570,573
FILING DATE: 20-AMAY-12
APPLICATION NUMBER: 09/187,319
FILING DATE: CURKNOWN>
APPLICATION NUMBER: 08/187,319
FILING DATE: CURKNOWN>
ATTORNEY AGGNIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 39,714
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEPHONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 226, Application US/09918715
Fublication No. US20030017157A1
GENERAL INFORMATION:
APPLICANT: Brad &t. Croix
APPLICANT: Bert Vogelstein
TILE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: 60/224,599
PRIOR PILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLONE: COLLAGEN ALPHA 1 (III)
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC STREET: 805 Third Avenue CITY: New York STATE: New York COUNTRY: USA ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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Best Local Similarity 100.
Matches 6; Conservative
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APPLICANT: Mills, Gordon B.

TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-039
CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT FILING DATE: 2002-06-21
PRIOR PELICATION NUMBER: US 60/299,887
PRIOR PELICATION NUMBER: US 60/301,572
PRIOR PELICATION NUMBER: US 60/301,572
PRIOR PELICATION NUMBER: US 60/306,501
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-09-25
PRIOR PELICATION NUMBER: US 60/365,002
PRIOR PELICATION NUMBER: US 60/365,585
PRIOR FILING DATE: 2002-03-05
PRIOR PELING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SOSTWARE: FREENCY FLING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SEQ ID NOS: 506
TENNOME. PRICES
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FILE REFERENCE: MPMO1-029P2RNM CURRENT APPLICATION NUMBER: US 60/339,971

PRIOR FILING DATE: 2002-03-05

NUMBER OF SEQ ID NOS: 228

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 33

LENGTH: 14466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33, Application US/10301822
; Publication Wo. US20030148410A1
; GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 6; Conservative
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, ORGANISM: Homo Sapiens
US-10-301-822-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1211 EKAGGF 1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EKAGGF 6
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US-10-301-822-33
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1 EKAGGF 6

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Search completed: September 18, 2004, 04:56:11 Job time: 29.4706 secs
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1211 EKAGGF 1216
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

September 18, 2004, 04:02:05; Search time 7.29412 Seconds (without alignments) 79:125 Million cell updates/sec

US-10-615-959-39 32 1 EKAGGF 6 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

hypothetical prote hypothetical prote probable membrane hypothetical prote collagen alpha 1(I hypothetical prote phosphoglycerate k phosphoglycerate k phosphoglycerate k phosphoglycerate k phosphoglycerate k hypochetical prote hypothetical prote hypothetical prote collagen alpha 1(I hypothetical prote hypothetical prote probable glycosyl conserved hypothet phosphoprotein pho probable NADPH deh hypothetical prote collagen alpha 1(I hypothetical prote hypothetical prote puative protein [i hypothetical prote probable membrane Description SUMMARIES B71719 H97716 F72308 CGHU7L H87376 A55804 S55482 KIHOG KIHOG A25567 A33792 B84702 B87269 T28687 B24785 G85360 S59856 E81134 B81885 S62941 C64034 S41067 C84639 Query Match Length DB 1028 1075 1440 1464 100.0 100.0 100.0 Score Result No. 

sepil AND Phopa	himothotical reste	TOTO TICATE DIOCE	Conserved hypother	bimothorias] prote	hypothetical prote	Calcium Channel al	Lactobacillus aba	calcium channel ar	To hears chains V	NAD(D) transhidrog	hymothetical proto	nhosnhohiatidina n	hynotherical prote			
C95843	G87644	F69209	R69218	T02366	T51792	T30535	AC1647	A37860	824663	AC3550	E90326	D72480	S76645	E72632	AB1038	
7	2	-	1 0	ı ĸ	10	~	~	~	7	8	2	N	7	~	7	
355	371	403	58.5	644	655	1559	1571	1852	115	120	124	140	147	223	231	
87.5	87.5	87.5	87.5	87.5	87.5	87.5	87.5	87.5	84.4	84.4	84.4	84.4	84.4	84.4	84.4	
28	28	28	28	28	28	28	28	28	27	27	27	27	27	27	27	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

# ALIGNMENTS

A;Gene: rpmB; RP099

ö Gaps .. 100.0%; Score 32; DB 2; Length 97; ilarity 100.0%; Pred. No. 8.9; Conservative 0; Mismatches 0; Indels Query Match
Best Local Similarity
6, Conserve

60 EKAGGF 65 1 EKAGGF 6 à g

RESULT 2

50S ribosomal protein L28 [imported] - Rickettsia conorii (strain Malish 7)
C.Species: Rickettsia conorii
R.Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rou G.Soience 293, 2093-2099, 2001
A.Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A.Reference number: A97700; MUID:21442074; PMID:11557893
A.Recession: H97716
A.Residues: preliminary
A.Molecule type: DNA
A.Residues: 1-97 - KUR>
A.Residues: 1-97 - KUR>
A.Cossa-references: GB:AE006914; PIDN:AAL02674.1; PID:g15619179; GSPDB:GN00173

100.0%; Score 32; DB 2; Length 97; 100.0%; Pred. No. 8.9; o; Indels ive 0; Mismatches 0; Indels 6; Conservative Query Match Best Local Similarity Matches 6; Conserv ò

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EKAGGF

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A; Molecule type: mRNA
A; Residues: 149-163, 'G', 164-240, 'D', 242-471, 'D', 473-487, 'L', 489, 'S', 491-613, 'Y', 615-634,'
A; Residues: 149-163, 'G', 164-240, 'D', 242-471, 'D', 473-487, 'L', 489, 'S', 491-613, 'Y', 615-634,'
A; Residues: 149-163, 'G', 163-241, 'NID: 929545; PIDN: CAA33387.1; PID: 9330045
A; Note: the authors' translation of residues 905-932 is inconsistent with the nucleotide R; Seyer, 'J.' M., Kanag, A.H.
B; Robenistry 16, 'NIS8-1164, 1977
A; Title: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptides A; Reference number: A90399; MUID: 77134724; PMID: 57335
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rosidues: 186-194 <MIL>
A;Cross-references: GB:S62925; NID:g386425; PIDN:AAD13937.1; PID:g4261637
A;Cross-references: GB:S62925; NID:g386425; PIDN:AAD13937.1; PID:g4261637
B;Chlodo, A.A.; Sillence, D.O.; Cole, W.G.; Bateman, J.F.
Biochem. J. 311, 939-943, 1995
A;Title: Abnormal type III collagen produced by an exon-17-skipping mutation of the COL39A;Reference number: S59511; WUID:96067614; PMID:7487954
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A; Residues: 302-423 <CHI>
A; Residues: 302-423 <CHI>
A; Cross-references: GB: 579877; NID: g1195576; PIDN: AAB35615.1; PID: g1195577
R; Cross-references: GB: 73404-3411, 1978
Biochemistry 17, 3404-3411, 1978
Biochemistry 17, 3404-3411, 1978
A; Title: Covalent structure of collagen: amino acid sequence of five consecutive CNBr pel
A; Reference number: A90414; MUID: 79000343; PMID: 687591
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A,Molecule type: protein
A,Residues: 399-675, N', 677-727 <SEY3>
A,Residues: 399-675, N', 677-727 <SEY3>
A,Experimental source: liver
R,Lee, B.; Vitale, E.; Superti-Furga, A.; Steinmann, B.; Ramirez, F.
B,Lee, B.; Vitale, E.; Superti-Furga, A.; Steinmann, B.; Ramirez, F.
A, Biol. Chem. 266, 5256-5259, 1991
A,Title: G to T transversion at position +5 of a splice donor site causes skipping of the A,Reference number: 155349; MUID:91161621; PMID:1672129
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A;Ratus: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 537-605 LEE>
A;Cross-references: GB:M59312; NID:g180815; PIDN:AAA52041.1; PID:g180816
A;Cross-references: GB:M59312; NID:g180815; PIDN:AAA52041.1; PID:g180816
B;Seyer, J.M.; Mainardi, C.; Kang, A.H.
Biochemistry 19, 1589-1589, 1980
A;Title: Covalent structure of collagen: amino acid sequence of alpha1 (III)-CB5 from ty
A;Reference number: A90438; MUID:80198282; PMID:6246925
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A; Residues: 728-895, 'A', 897-964 <SEY4>
A; Resperimental Bource: liver
R; Cole, W.G.; Chiodo, A.A.; Lamande, S.R.; Janeczko, R.; Ramirez, F.; Dahl, H.H.M.; Chan
J. Biol. Chem. 265, 17070-17077, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: sequence corrected by A94562; attachment of 2-0-alpha-D-glucosyl-O-beta-D-galacton R;Seyer, J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 'V',169-225,229-277,'A',279-292,'D',294,'S',296-398 <SEY2>
A;Experimental source: liver
A;Note: author submitted corrections to A90399
R;Milewicz, D.M.; Mitz, A.M.; Smith, A.C.; Manchester, D.K.; Waldstein, G.; Byers, P.H.
Am. J. Hum. Genet. S3, 62-70, 1993
A;Title: Parental somatic and germ-line mosaicism for a multiexon deletion with unusual
                                                                                                                                                                 A; Title: Nucleotide and amino acid sequences of the entire human alpha-1 (III) collagen. A; Reference number: $04887; MUID:89386015; PMID:2780304
A;Crobs-references: EMBL:X07240, NID:g30060; PIDN:CAA30229.1; PID:g30061 A;Note: the authors translated the codon CAG for residue 154 as His R;Janeczko, R.A.; Ramirez, F. Nucleic Acids Res. 17, 6742, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Reaidues: 'V',169-225,229-232,'P',234-292,'D',294-398 <SEYl>
A;Experimental source: liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Riseyer, J.M.
submitted to the Atlas, December 1977
A;Reference number: A94562
A;Accession: A94562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: I55349
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CGHU71

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Nature 399, 323-329, 1999
Nature Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Recession: F72308
A;Accession: F72308
A;Molecule type: DNA
A;Kesiduea: preliminary
A;Kesiduea: 1-1289 cARN>
A;Kesiduea: 1-1289 cARN>
A;Cross-references: GB:AE001761; GB:AE000512; NID:g4981529; PIDN:AAD36071.1; PID:g498153
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TW0992
                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: F72308
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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                                                                                                                                                                                                                                                                                                                    C;ŝpecies: Thermotoga maritima
C;bate: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
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Matches 6; Conservative
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A; Residues: 1-170 <TOM>
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Accession: S01726

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Matches 6; Conservative
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A; Residues: 950-1018, 'Y', 1020-1183, 'S', 1185-1466 <MAN>
A; Residues: 950-1018, 'Y', 1020-1183, 'S', 1185-1466 <MAN>
A; Cross-references: EMBL: X06700; NID: 9330633; PIDN: CRA29886.1; PID: 9330054
B; Seyer, J.M.; Kang, A.H.
B; Seyer, J.M.; Kang, A.H.
B; Seyer, J.M.; Kang, M.H.
B; Seyer, J.M.; Kang, M.H.
B; Seyer, J.M.; May, M.J.
B; Residues: 965-979, 'A', 981-984,' PS', 987,' QN', 990-1096,' P', 1098-1152,' AT', 1155,' S', 1157-A; Experimental source: liver
B; Exoidl, H.R.; Brinker, J.M.; May, M.; Pihlajaniemi, T.; Morrow, S.; Rosenbloom, J.; Mye Nucleic Acids Res. 12, 9383-9394, 1984
A; Title: Molecular cloning and carboxyl-propeptide analysis of human type III procollage
                           Б
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A; Residues: 1065-1155, 'P', 1157-1466 <LOI>
A; Residues: 1065-1155, 'P', 1157-1466 <LOI>
A; Residues: 1065-1155, 'P', 1157-1466 <LOI>
B; Cross-references: EMBL:X01655; EMBL:X01742; NID:929584; PIDN:CAA25821.1
R; Miskulin, M.; Dalgleish, R.; Kluve-Beckerman, B.; Rennard, S.I.; Tolstoshev, P.; Brant Biochemistry 25, 1408-1413, 1986
A; Title: Human type III collagen gene expression is coordinately modulated with the type A; Reference number: 152393; MUID:86187804; PMID:3754462
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Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
A; Title: Human alpha 1(III) and alpha 2(V) procollagen genes are located on the long arm
A; Reference number: I59025; MUID:85216505; PMID:3858826
                                                                                                                                                                                                                  PIDN:AAB59383.1; PID:g
with Ehlers-Danlos syz
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A;Map position: 2q31-2q31
A;Introns: 27/1; 94/3; 111/3; 149/3; 176/3; 554/3; 587/3; 1175/3; 1275/1; 1337/3; 1418/3
A;Note: the list of introns is incomplete; defects in this gene can result in Ehlers-Dan C;Complex: type III collagen is a homotrimer of monomers initially linked by disulfide her of their length, is formed with desmosine cross-links made from lysine and allysine r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Description: structural component of extracellular fibrous polymer that maintains inte
       Title: A base substitution at a splice site in the COL3A1 gene causes exon skipping Reference number: A38303; MUID:91009133; PMID:2145268
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A; Residues: 1165-1196 < EMA>
A; Residues: 1165-1196 < EMA>
A; Cross-references: GS-M1134; NID:g180417; PIDN:AAAS2004.1; PID:g180418
R; Chu, M.L.; Weil, D.; de Wet, W.; Bernard, M.; Sippola, M.; Ramirez, F.
J. Biol. Chem. 260, 4357-4363, 1985
A; Title: Isolation of cDNA and genomic clones encoding human pro-alphal(III) collagen.
A; Reference number: A92516; MUID:85157600; PMID:2579949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: liver A; Note: the authors translated the codons given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1176-1240, V',1242-1356,'P',1358-1466 <CHU>
A;Cross-references: GB:M10615; GB:M10793; GB:M10794; GB:M10795; GB:M10796; GB:M10797;
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A;Title: A base substitution at a splice site in the COL3Al gene causes A;Reference number: A38303; MUD:91009133; PMLD:2145268
A;Accession: A38303
A;Molecule type: MRNA
A;Residues: 861-1015 <COL>
A;Cross-references: GB:J05617; GB:M55603; GB:M59227; NID:g180878; PIDN
A;Cross-references: GB:J05617; GB:M55603; GB:M59227; NID:g180878; PIDN
A;Cross-references: GB:J05617; GB:M55603; GB:M59227; NID:g180878; PIDN
A;Mankoo, B.S.; Dalgleish; PA:A; 1988
A;Title: Human pro alphal(III) collagen: CDNA sequence for the 3' end.
A;Reference number: S02119; MUID:88189827; PMID:3357782
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A;Status: translated from GB/EMBL/DDBJ
M;Molecule type: mRNA
A;Residues: 1161-1200 <MIS>
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C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; C;Superfamily: collade coll; Ehlers-Danlos syndrome; extracellular matrix; glycoprotein; hydrowords: colled coll; Ehlers-Danlos syndrome; extracellular matrix; glycoprotein; F;1-23/Domain: signal sequence #status predicted <PRO> F;24-153/Domain: amino-terminal propeptide #status predicted <PRO> F;124-121/Product: collagen alpha 1(III) chain #status predicted <PRO> F;154-122/Product: collagen alpha 1(III) chain #status predicted <PRO> F;154-123/Region: amino-terminal nonhelical telopeptide
F;109-1093/Region: cellattachment (R-G-D) motif
F;109-1093/Region: cellattachment (R-G-D) motif
F;109-1093/Region: carboxyl-terminal nonhelical telopeptide
F;1227-1466/Domain: carboxyl-terminal propeptide #status predicted
F;123-1466/Domain: fibrillar collagen carboxyl: terminal homology <PCC> F;24/Modified site: pyrrolidone carboxyl: acid (GIn) (in mature form) #status predicted
F;153-154/Oodified site: pyrrolidone carboxylic acid (GIn) (in mature form) #status predicted
F;161,1212/Modified site: pyrrolidone carboxylic acid (GIn) (in mature form) #status F;161,1212/Modified site: carboxylate (Lys) #status experimental
F;263/Shinding site: carboxylate (Lys) (covalent) #status experimental
F;584,1094/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental
F;584,1094/Modified site: 5-hydroxylysine (Lys) (covalent) #status experimental
F;948-949/Cleavage site: Gly-Ile (collagenase) #status experimental
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Cibate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
Ciracession: H87376
Eibate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
Ciracession: H87376
Billie: Charle March M. T.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.E.
Billie: Cambiate, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolone
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: AB7249; MUID:21173698; PMID:11259647
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R;Klumpp, S.; Hanke, C.; Donella-Deana, A.; Beyer, A.; Kellner, R.; Pinna, L.A.; Schultz, J. Biol. Chem. 268, 32744-32780, 1994

A;Title: A membrane-bound protein phosphatase type 2C from Paramecium tetraurelia. Purif; A;Reference number: A55804; MUID:95105156; PMID:7806499

A;Status: preliminary
A;Nolecule type: mRNA
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C.Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 07-Dec-1999
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C, Comment: Residues thought to be involved in ADP-ATP binding are Glu-343 to ribose and
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                                                                                                                                                                                                                                                                                              Query Match 90.6%;
Best Local Similarity 83.3%;
Matches 5; Conservative
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Residues: 1-14 <RES>
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C; Species: Equus caballus (domestic horse)
C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 28-Feb-1997
C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 28-Feb-1997
C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 28-Feb-1997
C; Accession: A92292; A00669
R; Marrett, M.
J. Biol. Chem. 256, 10293-10305, 1981
A; Mill: Date sequence of the enzyme.
M; Reference number: A92292; MUID: 82030789; PMID: 7287713
A; Reference number: A92292; MUID: 82030789; PMID: 7287713
A; Molecule type: protein
A; Residues: 1-416 <MER>
R; Banks, R.D.; Blake, C.C.F.; Evans, P.R.; Haser, R.; Rice, D.W.; Hardy, G.W.; Merrett, Nature 279, 773-777, 1979
A; Till: Sequence, structure and activity of phosphoglycerate kinase: a possible hinge-ha; Reference number: A93209; MUID: 7919779; PMID: 4503209; MUID: 7919799; PMID: 4503209; MUID: 7919799; PMID: 4503209; MUID: 7919779; MUID: 7919799; PMID: 4503209; MUID: 79197999; PMID: 4503209; MUID: 7919799; PMID: 4503209; MUID: 7919799; MUID: 7919799; MUID: 7919799; MUID: 7919799; MUID: 7919799; MUID
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A; Residues: 1-382 <CO2>
A; Cross-references: EMBL:249811; PIDN:CAA89954.1; GSPDB:GN00066; SPDB:SPAC5H10.04
A; Experimental source: strain 972h-; cosmid c5H10
C; Genetics: SPDB:SPAC5H10.04
A; A; Gene: SPDB:SPAC5H10.04
A; Map position: 1
C; Superfamily: NADPH dehydrogenase chain OYE2
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R;Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, May 1995
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                                                                  A;Cross-references: GB:Z36985; NID:g537421; PID:e1192609; PID:g2654382 C;Genetics: A;Genetic code: SGC5 C;Keywords: phosphoric monoester hydrolase
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83.3%; Pred. No. 1.4e+02;
:ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                     Similarity 83.3%; Score 29; DB 2; Length 300 Similarity 83.3%; Pred. No. 1.1e+02; 5; Conservative 1; Mismatches 0; Indels
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A,Accession: T38968
A,Status: preliminary; translated from GB/EMBL/DDBJ
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R, Connor, R.; Churcher, C.M.
submitted to the EMBL Data Library, May 1995
A, Reference number: S55479
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Matches 5; Conservative
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175 ERAGGF 180
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Matches 5; Conserv
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-382 <CON>
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EKSGGF 71
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                                             A;Residues: 1-300 <KLU>
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A;Molecule type: mRNA
A;Residues: 1-417 <MIC>
A;Cross-references: GB:J00160; GB:J00288; NID:g189904; PIDN:AAA60078.1; PID:g387020
A;Cross-references: GB:L00160; GB:J00288; NID:g189904; PIDN:AAA60078.1; PID:g387020
A;Experimental source: live: Noshida, A.
B;Huang, I.Y.; Welch, C.D.; Yoshida, A.
B;Ol. Chem. 255, 6412-6420, 1980
A;Title: Complete amino acid sequence of human phosphoglycerate kinase. Cyanogen bromide A;Reference number: A92279; MUID:80227775; PMID:7391027
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R;Singer-Sam, J.; Keith, D.H.; Tani, K.; Simmer, R.L.; Shively, L.; Lindsay, S.; Yoshida, Gene 32, 409-417, 1984
A;Title: Sequence of the promoter region of the gene for human X-linked 3-phosphoglycerat A;Reference number: A2426; MUID:8515567; PMID:6099325
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C;Comment: The structure consists of two discrete, globular domains that are joined by r
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A; Molecule type: protein
A; Residues: 2-39, K', 40-52, 'D', 54-109, 'D', 111-275, 'D', 277-299, 'E', 301-336, 'D', 338-385, 'Q
A; Experimental source: erythrocytes
R; Jindal, H.K.; Vishwanatha, J.K.
J; Biol. Chem. 265, 6540-6543, 1990
A; Title: Functional identity of a primer recognition protein as phosphoglycerate kinase.
A; Reference number: A35739; MUID:90216667; PMID:2324090
A; Accession: A33739
39-341.
C;Superfamily: phosphoglycerate kinase
C;Superfamily: phosphotransferase
C;Superfamily: phosphotransferase
C;Keywords: acetylated amino end (Ser) #status experimental
F;1/Modified site: acetylated amino end (Ser) #status experimental
F;219,343/Binding site: ATP (Lys, Glu) #status experimental
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A; Residues: 1-21 <SIN>
R; Pfeifer, G.P.; Steigerwald, S.D.; Mueller, P.R.; Wold, B.; Riggs, A.D.
Science 246, BlO-813, 1989
A; Title: Genomic sequencing and methylation analysis by ligation mediated PCR.
A; Reference number: IS9539; MUID:90049205; PMID:2814502
A; Accession: IS9539
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A,Status: translated from GB/EMBL/DDBJ
A,Rolecule type: DNA
A,Rosidues: 1-417 -RRE2.
A,Rossidues: 1-417 -RRE2.
A,Rossidues: GB:M11968; NID:g189920; PIDN:AAA60079.1; PID:g387021
R,Michelson, A.M.; Markham, A.F.; Orkin, S.H.
Proc. Natl. Ascid. Sci. USA. 80, 472-476, 1983
A,Fitle: Isolation and DNA sequence of a full-length cDNA clone for human X A,Reference number: A93962; MUID:83169680; PMID:6188151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 14-Nov-1983 #sequence revision 23-Aug-1996 #text change 24-Sep-1999
C;Accession: 159050; A00669; A92279; A35739; A2426; 159539
C;Accession: 159050; A00669; A92279; A35739; A72426; 159539
Proc. Natl. Acad. Sci. U.S.A. 82, 6955-6959; 1985
A;Title: Structure of the human phosphoglycerate kinase gene and the intron-A;Reference number: 159050; MUID:86016816; PMID:2995995
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                            Score 29; DB 1; Length 416;
Pred. No. 1.5e+02;
1; Mismatches 0; Indels
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phosphoglycerate kinase (EC 2.7.2.3) - Chinese hamster Cisceulus griseus (Chinese hamster) (Cibate: Criceulus griseus (Chinese hamster) (Cibate: O2-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999 (Cibacession: 148074 N.F.; Morgan, M.J.; Faik, P. Rifassan-Malker, A.F.; Morgan, M.J.; Faik, P. Asman-Roll Mol. Genet. 21, 75-81, 11995 for glucose phosphate isomerase and phosphoglyceficient variant of CHO-KI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Rattus norvegicus (Norway rat)
C;bate: 23-Mar-1990 #text_change 18-Jun-1999
C;bate: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 18-Jun-1999
C;Accession. A33792
R;Ciccarese, S.; Tommasi, S.; Vonghia, G.
B;Ciccarese, S.; Tommasi, S.; Vonghia, G.
A;Citle: Cloning and cDNA sequence of the rat X-chromosome linked phosphoglycerate kinase
A;Reference number: A33792
A;Reference number: A33792
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Rolecule type: mRNA
A,Rosidues: 1-417 <RES>
A,Cross-references: EMBL:Z37974; NID:9987047; PIDN:CAA86028.1; PID:9987048
C,Superfamily: phosphoglycerate kinase
C,Superfamily: phosphoglycerase
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
                                                                                                                                                                                Gaps
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             C;Superfamily: phosphoglycerate kinase
C;Keywords: ATP; gluconeogenesis; glycolysis; phosphotransferase
                                                                                                                 Length 417;
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                                                                                                             Score 29; DB 2; Le
Pred. No. 1.5e+02;
1; Mismatches 0;
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83.3%; Pred. No. 1.5e+02;
live 1; Mismatches 0;
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Pred. No. 1.5e+02;
1; Mismatches 0
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                                                                                                             90.6%;
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 83.33
Matches 5; Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
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183 QKAGGF 188
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A;Molecule type: mRNA
A;Residues: 1-417 <CIC>
                                                                                                                                                                                                                                        1 EKAGGF 6
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                                                                                                                 A;Gene: GDB:PGK1
A;Cross-references: GDB:120282; OMIM:311800
A;Map position: Xq13.3-Xq13.3
A;Introns: 22/2; 39/2; 31/2; 139/3; 174/2; 214/2; 252/3; 312/3; 372/1; 405/1
C;Superfamily: phosphoglycerate kinase
C;Keywords: ATP; blocked amino end; gluconeogenesis; glycolysis; phosphotransferase
C;Keywords: ATP; blocked amino end; Gsr) (in mature form) (probably acetylated) #statu
F;220,344/Binding site: ATP (Lys, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphoglycerate kinase (EC 2.7.2.3) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1998 #sequence revision 30-Jun-1998 #text_change 18-Jun-1999
C;Accession: A25567; A29613; $21393; 148708; 148710
R;Mori, N.; Singer-Sam, J.; Lee, C.Y.; Riggs, A.D.
A;Title: The nucleotide sequence of a cDNA clone containing the entire coding region for A;Reference number: A25567; MUID:87106824; PMID:3542714
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A;Residues: 1-22 <ADR>
A;Residues: 1-22 <ADR>
K;Boer, P.H.; Potten, H.; Adra, C.; Jardine, K.; Mllhofer, G.; McBurney, M.
submitto the EMBL Data Library, May 1989
A;Description: The mouse pgk-1 promoter induces efficient gene expression: identification
A;Reference number: S21393
406-417 form a helix associated with the amino-terminal domain.
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A,Residues: 1-21 <BOB.
A,Residues: 1-21 <BOB.
A,Cross-references: BMBL:X15339; NID:g53671; PIDN:CAA33391.1; PID:g53672
B,Tamaru, M.; Nagao, Y.; Taira, M.; Tatibana, M.; Masamune, Y.; Nakanishi, Y.
Biochim. Biophys. Acta 1049, 331-338, 1990
A,Title: Selective activation of testis-specific genes in cultured rat spermatogenic cell A;Reference number: 148708; MUID:90344879; PMID:2166582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-417 < MOR>
A; Residues: 1-417 < MOR>
A; Cross-references: GB:W15668; NID:g202422; PIDN:AAA70267.1; PID:g202423
A; Cross-references: GB:W15668; NID:g202422; PIDN:AAA70267.1; PID:g202423
A; Note: the authors translated the codon AAC for residue 56 as Lys
B; Adra, C.N.; Boer, P.H.; McBurney, M.W.
Gene 60, 65-74, 1987
A; Aitle: Cloning and expression of the mouse pgk-1 gene and the nucleotide sequence of A; Reference number: A29613; MUID:88152503; PMID:3440520
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A/Reference number: 148710; MUID:90365677; PMID:1975492
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A;Residues: 1-21 <RES>
A;Cross-references: EMBL:X55309; NID:g57875; PIDN:CAA39013.1; PID:g57876
A;Cross-references: EMBL:X55309; NID:g57875; PIDN:CAA39013.1; PID:g57876
B;Boer, P.H.; Potten, H.; Adra, C.N.; Jardine, K.; Mullhofer, G.; McBurney, M.W.
Biochem. Genet. 28, 299-308, 1990
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A;Molecule type: DNA
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Best Local Similarity 83.37
Best Local Si Conservative
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183 QKAGGF 188
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A;Introns: 22/2
                                                                                                Genetics:
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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
Nature 402, 761-768, 1999
A;Ritle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUD:20083487; PMID:10617197
A;Accession: B84702
A;Accession: B84702
A;Accession: B84702
A;Accession: B84702
A;Accession: B848702
A;Accession: B848702
A;Accession: B848702
A;Cross-references: GB:AE002093; NID:g4567216; PIDN:AAD23631.1; GSPDB:GN00139
C;Genetics:
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BB8726
hypothetical protein CC0163 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Date: 20-Apr-2001
Bsecont Resequence_revision 20-Apr-2001 #text_change 20-Apr-2001
R;Micran, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
Br.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
H. J.; Erndlaevar, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: AB97249; MUID:21173698; PMID:11259647
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T28697
hypothetical protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C;Accession: T28687
R;Parkhill, J; Bentley, S.D.; Barrell, B.G.; Rajandream, M.A.
R;Parkhill, J; Bentley, S.D.; Barrell, B.G.; Rajandream, M.A.
A;Reference number: Z20512
A;Recession: T28687
A;Recession: T28687
A;Recule type: DNA
A;Redule type: DNA
A;Residues: 1-52 < ARR>
A;Residues: 1-52 < ARR>
A;Residues: 1-52 < ARR>
A;Ressereferences: EMBL:AL023496; PIDN:CAA18904.1
C;Superfamily: Escherichia coli probable transport protein b0511
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A;Cross-references: GB:AE005673; NID:g13421278; PIDN:AAK22150.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC0163
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A;Map position: 2
C;Superfamily: Arabidopsis thaliana hypothetical protein F17J16.30
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90.6%; Score 29; DB 2; Length 522;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels
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Pred. No. 1.5e+02;
1; Mismatches 0; Indels
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A, Status: preliminary
A, Molecule type: DNA
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Search completed: September 18, 2004, 04:30:48 Job time : 12.2941 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

September 18, 2004, 03:48:54; Search time 4.47059 Seconds (without alignments) 69.884 Million cell updates/sec Run on:

US-10-615-959-39 32 1 EKAGGF 6 Title: Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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21	28	87.5		Н	CCAS CYPCA	_
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25	27	84.4	344	-	DCUP BRAJA	
56	27	84.4	373	н	DMT1_PIG	
27	27	84.4	373	Н	Y085 METJA	_
28	27	84.4	379	Н	O71A_DROME	_
29	27	84.4	379	П	YG36 METMA	_
30	27	84.4	388	П	TRM1 METAC	
31	27	84.4	393	Н	S17P_ARATH	
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33	27	84.4	420	Н	CT13_MOUSE	11 mus

Q9a5bB caulobacter P45679 coxiella bu Q9x4g0 pseudomonas Q9s306 ruminococcu p00944 escherichia P29442 klebsiella Q9x1z5 thermotoga P75832 bacillus li P00970 bacteriopha P19088 bacteriopha O93532 gallus gall	ALIGNMENTS  STANDARD; PRT; 97 AA.  1. 41, Last sequence update)  1. 50 Rocteria; Alphaproteobacteria; Rickettsiales;  1. 8. Renesto-Audiffren P., Fournier PE., Barbe V., V., Cossart P., Weissenbach J., Claverie JM.,  1. Volution in Rickettsia conorii and R. prowazekii.";  2098 (2001)  1. 8 Floss family of ribosomal proteins.  1. 10 Rochest Statement of Bioinformatics and the EMBL outstation in Statement is not removed. Usage by and for commercial static institutions as its content is in no way static incense agreement (See http://www.isb-sib.ch/announce/  1. 10 license@isb-sib.ch)  1. 41, Last sequence update)  1. 41, Last sequence update)  1. 41, Last sequence update)  1. 5 Rockettsiales  2. 6 Rockettsiales  3. 7 Rockettsiales  4. 6 Rockettsiales  5. 8 Institute of Bioinformatics and the EMBL outstation in the intermed as long as its content is in no way as tactement is not removed. Usage by and for commercial staticness also connected in the intermed of the intermed is in the intermed of the intermed is in the intermed of the intermed intermed intermed is intermed	C CRC64,
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4 4 3 2 5 4 4 4 5 6 5 4 4 5 6 5 4 4 5 6 5 6 5 4 5 6 5 6	1 CCN 128 RICCN 92071,	TIAN, MP 00373; -; 1. INTELPIO, IPR00138; Ribosomal Pfam; PF00830, Ribosomal L28; TIGRPAMs; TIGR0009; L28; 1. Ribosomal protein; Complete pr SEQUENCE 97 AA; 10766 MW;
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Gaps .; 0 Query Match
Best Local Similarity 100.0%; Score 32; DB 1; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 6; Conservative 0; Mismatches 0; Indels 1 EXAGGF 6 à

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RESULT 2
RL28 RICPR
LD RL28RICPR STANDARD; PRT; 97 AA.
AC 092E48;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

97 AA.

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SEQUENCE OF 1-170 FROM N.A.
(III) collagen.";
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                     STRAIN=Madrid E;
MEDLINE=99039499;
Andersson J.O.,
Anderson S.G. E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
Sicheritz-Ponten T., Minkler H.H., Kurland C.G.,
"The genome sequence of Rickettsia prowazekii and the origin of
mitochondria.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                  Nature 396:133-140(1998).
-!- SIMILARITY: Belongs to the L28P family of ribosomal proteins.
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                                                            Rickettsia prowazekii.
Bacteria; Proteobacteria; Alphaproteobacteria, Rickettsiales;
Rickettsiaceae; Rickettsleae; Rickettsia.
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MEDLINE=89350838; PubMed=2764886;
Ala-Kokko L., Kontusaari S., Baldwin C.T., Kuivaniemi H.,
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21-UUL-1986 (Rel. 01, Created)
01-UAN-1990 (Rel. 13, Last sequence update)
01-CCT-2003 (Rel. 42, Last annotation update)
Collagen alpha 1(III) chain precursor.
      annotation update)
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PIR; B71719; B71719.
HAMAP; MF 00373; -; 1.
InterPro; IPR001383; Ribosomal L28.
Pfam; PF00830; Ribosomal L28; 1.
TIGRFAMS; TIGR0009; L28; 1.
Ribosomal protein; Complete proteone.
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                                                                                                                               NCBI_TaxID=782;
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Chu M.-L., Weil D., de Wet W.J., Bernard M.P., Sippola M., Ramirez F., "Isolation of cDNA and genomic clones encoding human pro-alpha 1 (III) collagen. Partial characterization of the 3' end region of the qene.";
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                                                                                                   MEDLINE=77134724; PubMed=557335;
Seyer J.M., Kang A.H.;
Seyer J.M., Kang A.H.;
"Covalent structure of collagen: amino acid sequence of cyanogen
bromide peptides from the amino-terminal segment of type III collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDINE-86187804; PubMed=3754462; Miskulin M., Dalgleish R., Kluve-Beckerman B., Rennard S.I., Miskulin M., Dalgleish R., Kluve-Beckerman B., Rennard S.I., Tolstoshev P., Brantly M., Crystal R.G.; "Human type III collagen gene expression is coordinately modulated with the type I collagen genes during fibroblast growth."; Biochemistry 25:1408-1413 (1986).
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Seyer J.M., Kang A.H.;
Covalent structure of collagen: amino acid sequence of five consecutive CNBr peptides from type III collagen of human liver.";
Biochemistry 17:3404-3411(1978).
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MEDLINE=8818987; PubMed=3357782;
Mankoo B.S., Dalgleish R.;
"Human pro alpha 1(III) collagen: cDNA sequence for the 3' end.";
Nucleic Acids Res. 16:2337-2337(1988).
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Molyneux K., Dalgleish R.;
"Human type III collagen 'variant' is a cDNA cloning artefact.";
Nucleic Acids Res. 16:11833-11833 (1988).
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Seyer J.M., Mainardi C., Kang A.H.;
"Covalent structure of collagen: amino acid sequence of alpha 1
(III)-CBs from type III collagen of human liver.";
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MEDLINE=81208139; PubMed=7016180;
Seyer J.M., Kang A.H.;
Covalent structure of collagen: amino acid sequence of alpha 1(III)-CB9 from type III collagen of human liver.";
Biochemistry 20:2621-2627(1981).
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Submitted (DEC-1977) to the PIR data bank.
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Nucleic Acids Res. 17:6742-6742(1989)
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MEDLINE=85157600; PubMed=2579949;
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MEDLINE=89098346; PubMed=3211760;
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MEDLINE=9329398 PubMed=8514866;

Tromp G., Wu Y., Prockop D.J., Madhatheri S.L., Kleinert C.,

Barley J.J., Zhuang J., Noerrgaard O., Darling R.C., Abbott W.M.,

Cole C.W., Jaakkola P., Ryynaenen M., Pearce W.H., Yao J.S.T.,

Majamaa K., Smullens S.N., Gatalica Z., Ferrell R.E., Jimenez S.R.,

Jackson C.E., Michels V.V., Kaye M., Kuivaniemi H.;

Sequencing of cDNA from 50 unrelated patients reveals that mutations in the triple-helical domain of type III procollagen are an infrequent cause of aortic aneurysms.";
                                                                                                                                                                                                                                                                                                                 Kuivaniemi H., Tromp G., Prockop D.J.;
"Mutations in fibrillar collagens (types I, II, III, and XI), fibril-
associated collagen (type IX), and network-forming collagen (type X)
cause a spectrum of diseases of bone, cartilage, and blood vessels.";
Hum. Mutat. 9:300-315(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kontusaari S., Tromp G., Kuivaniemi H., Romanic A.M., Prockop D.J.; "A mutation in the gene for type III procollagen (COL3A1) in a family with aortic aneurysms.";
                                      Toman D., Ricca G., de Crombrugghe B.,
"Nucleotide sequence of a cDNA coding for the amino-terminal region
of human prepro alpha 1(III) collagen.";
Nucleic Acids Res. 16:7201-7201(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT THR-698.
MEDLINE=91045136; PubMed=2235526;
Zafarullah K., Kleinert C., Tromp G., Kuivaniemi H., Kontusaari S., Wu Y., Ganguly A., Prockop D.J.;
"G to A polymorphism in exon 31 of the COL3A1 gene.";
Nucleic Acids Res. 18:6180-6180(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=89109135; PubMed=2492273;
Tromp G., Kuivaniemi H., Shikata H., Prockop D.J.;
"A single base mutation that substitutes serine for glycine 790 of the alpha 1 (III) chain of type III procollagen exposes an arginine and causes Ehlers-Danlos syndrome IV.";
"Biol. Chem. 264:1349-1352(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tromp G., de Paepe A., Nuytinck L., Madhatheri S.L., Kuivaniemi H., "Subbstitution of valine for glycine 793 in type III procollagen in EMlers-Danlos syndrome type IV.";
Hum. Mutat. 5:179-181(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Richards A.J., Narcisi P., Lloyd J.C., Ferguson C., Pope F.M.; "The substitution of glycine 661 by arginine in type III collagen produces mutant molecules with different thermal stabilities and causes Ehlers-Danlos syndrome type IV."; Med. Genet. 30:690-693(1993).
                                                                                                                                                                              Benson-Chanda V., Su M.W., Weil D., Chu M.-L., Ramirez F.; "Cloning and analysis of the 5' portion of the human type-III procollagen gene (COL3A1)."; Gene 78:255-265(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT AORIIC ANEURYSM ARG-303, AND VARIANT THR-668.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clin. Invest. 86:1465-1473(1990).
                                                                                                                                         FROM N.A.
PubMed=2777083;
                                                                                                                                                                                                                                                                                                 MEDLINE=97255959; PubMed=9101290;
  TISSUE=Placenta;
MEDLINE=88303360; PubMed=3405773;
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MEDLINE=91056145; PubMed=2243125;
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MEDLINE=94016385; PubMed=8411057;
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                                                                                                                                           1-176
                                                                                                                                                       MEDLINE=89378752;
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                                  "A single base mutation in the gene for type III collagen (COL3A1) converts glycine 847 to glutamic acid in a family with Ehlers-Danlos syndrome type IV. An unaffected family member is mosaic for the
                                                                                                                                               WARIANT EDS-IV ASP-1050.
MEDLINE=90037070; PubMed=2808425;
Tromp G., Kuivaniemi H., Stolle C.A., Pope F.M., Prockop D.J.;
"Single base mutation in the type III procollagen gene that converts the codon for glycine 881 to aspartate in a mild variant of Ehlers-Danlos syndrome IV.";
J. Blol. Chem. 264:19313-19317(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                  "Characterisation of a glycine to valine substitution at amino acid position 910 of the triple helical region of type III collagen in a patient with Enhers-Danlos syndrome type IV."; J. Med. Genet. 28:458-463 [1991].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphate.
-!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
-!- SUBCELLULAR LOCATION: Membrane-bound.
Richards A.J., Ward P.N., Narcisi P., Nicholls A.C., Lloyd J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
                                                                                                                                                                                                                                                                                                                           MEDLINE=91374480; PubMed=1895316;
Richards A.J., Lloyd J.C., Ward P.N., de Paepe A., Narcisi P.,
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MBDLINE=95105156; PubMed=7806499;
Klumpp S., Hanke C., Donella-Deana A., Beyer A., Kellner R.,
Pluna L.A., Schultz J.E.,
"A membrane-bound protein phosphatase type 2C from Paramecium
tetraurelia. Purification, Characterization, and cloning.";
J. Biol. Chem. 265:32774-32780(1994).
--- FUNCTION: Enzyme with a broad specificity.
--- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 32; DB 1; Length 1466; 100.0%; Pred. No. 51; ative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93022543; PubMed=1357232;
Johnson P.H., Richards A.J., Pope F.M., Hopkinson D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O1-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Dast sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein phosphatase 2C (EC 3.1.3.16) (PP2C)
Paramecium tetraurelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300 AA
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-!- SIMILARITY: Belongs to the PP2C family.
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                                                                                                               Hum. Genet. 89:414-418(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                      Pope F.M.;
                                                                                               mutation."
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NCBI_TaxID=4896;
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Q09670;
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"Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermithis.";

Nat. Biotechnol. 21:226-531(2003).

-!- FUNCTION: The glycine cleavage system catalyzes the degradation of glycine (By similarity).

-!- CATALYTIC ACTIVITY: (6S)-tetrahydrofolate + S-
aminomethyldihydrolipoy/brotein = (6R)-5,10-
methylenetetrahydrofolate + NH(3) + dihydrolipoylprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: The glycine cleavage system is composed of four proteins: P, T, L and H (By similarity).
-!- SIMILARITY: Belongs to the gcvT family.
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                       MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 (BY SIMILARITY).
MANGANESE 1 AND 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
MANGANESE 2 (BY SIMILARITY).
BC0318B4FF7724BC CRC64;
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SETAINE-MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE-21477403; PubMed=11572948;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                  0820I2;
10-CCT-2003 (Rel. 42, Created)
10-CCT-2003 (Rel. 42, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Aminomethyltransferase (EC 2.1.2.10) (Glycine cleavage system
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                         DB 1; Length 300;
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MEDLINE=22608306; PubMed=12692562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                           90.6%; Score 29;
  send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                 Hydrolase; Magnesium; Manganese;
                                               HSSP, P35813; 1A6Q.
InterPro; IPR001932; PP2C-like.
InterPro; IPR000222; PP2C.
Pfam; PF00481; PP2C; 1.
SMART; SM00331; PP2Cc; II.
PROSITE; PS01032; PP2C; 1.
                                                                                                                                                                                                    33739 MW;
                           EMBL; Z36985; CAA85448.1; -.
                                                                                                                                                                                                                                                   5; Conservative
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                                       PIR; A55804; A55804.
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300 AA;
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ERAGGF 180
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                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metabolites.";
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RC STRAIN=972;

RA MEDLINE=21848401; PubMed=11859360;

RA WEDLINE=21848401; PubMed=11859360;

RA WOOD V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., RA Gools J., Brown B., Basham D., Bowman S., Chillingworth T., Churcher C.M., RA Gools K., Brown D., Park S., Hollingworth T., Churcher C.M., RA Gentles S., Goble A., Hamin N., Harris D., Hidalgo J., Hodgson G., Relived S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K., RA Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K., RA Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K., RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Nolle S., Mungall K., Murphy L., Niblett D., Odell C., Ra McDons P., Saudnders D., Seeger K., Sharp S., Stucher K., Stamon R., Stamon R., Stunders B., States S., Stevens K., States S., Stevens K., States S., Stevens K., States S., Stevens K., Arylor K., Taylor R.G., Tivey A., Walsh S.V., Wairen T., Whitehead S., Mochard J., Volckaert G., Aert R., Robben J., Grymonprez B., Aglein S., Langer I., Vanstreels B., Rieger M., Schaefer M., Mealler H., Reinhardt R., Pohl T.M., Reger P., Zimmermann W., Wedler H., Reinhardt R., Pohl T.M., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., RA, Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Aglibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Accrutti E., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Ra Accrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Cornelle J.L., Jimenez J., Sanchez M., Balbern I., Potashkin J., Ra Martin L., Lowe T., McCombie W.R., Paulsen I., Patached G., Nark, Wall R., McCombie W.R., Ranger D., Hurse S., R., Rather B., Reliner S., Rather B., Reliner S., Sancher R., Reliner S., Sanc
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01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative NADPH dehydrogenase C5H10.04 (EC 1.6.99.1) (Old yellow enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- CATALYTIC ACTIVITY: NADPH + acceptor = NADP(+) + reduced acceptor
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                                                                                                                                                                                                                                                                                                                                                 HAMAP, MF 00259; -: 1.
InterPro; IPR00622; GCV T.
InterPro; IPR006223; GCVT.
Pfam; PF01571; GCV T; 1.
TIGRFAMS; TIGR00528; GCVT; 1.
Transferase; Aminotransferase; Complete proteome.
SEQUENCE 372 AA; 39087 MW; DAAEC8E02547176F CRC64;
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-!- SUBUNIT: Homodimer or heterodimer (By similarity)
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Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No
                                                                                                                                                                                                                                                                                                  EMBL; AP005032; BAC70484.1; -.
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Best Local Similarity 83.3%;
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                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning and expression of the mouse pgk-1 gene and the nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=87106824; PubMed=3542714;
Mori N., Singer-Sam J., Lee C.-Y., Riggs A.D.;
"The nucleotide sequence of a cDNA clone containing the entire cregion for mouse X-chromosome-linked phosphoglycerate kinase.";
                                                                                                                                            PIR, S55482; S55482.
HSSP, Q02899; LOYC.
GeneDB_SPombe, SPACF110.04; -.
InterPro, IPR001155; Oxidored FMN.
Pfam; PF00724; oxidored FMN, I.
Hypothetical protein; Oxidoreductase; NADP; Flavoprotein; FMN;
                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISCUSSION OF SEQUENCE.
MEDLINE=86275275; PubMed=3525226;
Mori N., Singer-Sam J., Riggs A.D.;
"Evolutionary conservation of the substrate-binding cleft of
                                                                                                                                                                                                                                                                                                  Score 29; DB 1; Length 382;
Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-20 FROM N.A.
MEDLINE=90365677; PubMed=1975492;
BOER P.H., Potten H., Adra C.N., Jardine K., Mullhofer G.,
McBurney M.W.;
                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                   382 AA; 43813 MW; 3F7939599CA167D1 CRC64;
                                                                                                                                                                                                                                                                                                                                      ;
0
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01-OCT-1989 (Rel. 12, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
PGKI OR PGK-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    416 AA
                                                                                                                                                                                                                                                                                                                                1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-20 FROM N.A.
MEDLINE-88152503; PubMed=3440520;
Adra C.N., Boer P.H., McBurney M.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                  h
Similarity 83.3%;
5; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'EBS Lett. 204:313-317(1986).
                                                                                                                                EMBL; Z49811; CAA89954.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence of its promoter.";
Gene 60:65-74(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphoglycerate kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 spermatogenic cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 ||:|||
66 EKSGGF 71
                                                                                                                                                                                                                                                                                                                                                                 1 EKAGGF 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                  Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGK1 MOUSE
                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGK1_MOUSE
                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SY WE BERRY BERRY SECOND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
Polymorphisms in the coding and noncoding regions of murine Pgk-1
                                                                                                                           -!- SIMILARITY: Belongs to the phosphoglycerate kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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-!- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-phospho-D-glyceroyl phosphate.

-!- PATHWAY: Second phase of glycolysis; second step.
-!- SUBUNIT: Monomer.
-!- SUBUNIT: Belongs to the phosphoglycerate kinase family.
                               Biochem. Genet. 28:299-299(1990).
-1- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP phospho-D-glyceroyl phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Match 90.6%; Score 29; DB 1; Length 416; Local Similarity 83.3%; Pred. No. 70; les 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90121246; PubMed=2610697;
Cicarese S., Tommasi S., Vonghia G.;
"Cloning and cDNA sequence of the rat X-chromosome linked
phosphoglycerate kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     416 AA; 44405 MW; 8B879E5AD7E69E15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphoglycerate kinase, testis specific (BC 2.7.2.3).
PGK2 OR PGK-2.
                                                                                        -1- PATHWAY: Second phase of glycolysis; second step-1- SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P00566; 10PG.
WINSA-ZDRAGE; P00411; MOUSE.
MGD; MGI: 9755; Pgkl.
InterPro; IPR01576; PGK.
PRIMTS; PR00477; PHGLYCKINASE.
PROSITE; PS00111; PGLYCERATE KINASE; 1.
Transferase; Kinase; Multigene family; Glycolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1990 (Rel. 15, Created)
                                                                                                                                                                                                                                                                                                                  EMBL; M15668; AAA70267.1; -. EMBL; M18735; AAA39919.1; -. EMBL; X55309; CAA33913.1; -. EMBL; X15339; CAA33391.1; -. PIR; A25567; A25567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 QKAGGF 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EKAGGF 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                   alleles.";
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SEQUENCE
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P16617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Gaps

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Indels

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Pred. No. 70; 1; Mismatches

83.3%;

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5; Conservative
                                                                                                      182 OKAGGF 187
  Best Local Similarity
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                                                            1 EKAGGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Merrett M.;
                                                                                                                                                                                                            PGK HORSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BINDING
BINDING
SEQUENCE
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PGK1_HUMAN
                                                                                                                                                                  RESULT 10
PGK HORSE
                       Matches
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hassan A.F., Morgan M.J., Faik P., "Characterization of cDNAs coding for glucose phosphate isomerase and phosphoglycerate kinase in Chinese hamster ovary cell line CHO-Kl and identification of defects in R1.1.7, a glycolysis-deficient variant
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cricetulus griseus (Chinese hamster).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Somet. Cell Mol. Genet. 21:75-81(1995).

-!- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-phospho-D-glyceroy1 phosphate.

-!- PATHWAY: Second dass of glycolysis; second step.

-!- SUBUNIT: Monomer (By similarity).

-!- SUBUNIT: Belongs to the phosphoglycerate kinase family.
                                                                                                                                                                                                                                                                                                1; Length 416;
                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
7DCD55E0940242C5 CRC64;
                                                                                                                                                                                                                                                         416 AA; 44423 MW; 991EEC54432FA8DB CRC64;
                                                                                                                                                                    PRINTS; PRO0477; PHGLYCKINASE.
PROSITE; PS00111; PGLYCERATE_KINASE; 1.
Transferase; Kinase; Multigene family; Glycolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  416 AA
                                                                                                                                                                                                                                                                                            DB 70;
                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00111; PGLYCERATE_KINASE; 1.
                                                                                                                                                                                                                                                                                                  90.6%; Score 29;
83.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphoglycerate kinase (EC 2.7.2.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Ovary;
MEDLINE=95328037; PubMed=7604358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transferase, Kinase, Glycolysis.
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InterPro; IPRO01576; PGK.
Pfam; PF00162; PGK; 1.
PRINTS; PR00477; PHGLYCKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         416 AA; 44431 MW;
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                                                                     EMBL; M31788; AAA41838.1; -.
                                                                                         PIR; A33792; A33792.
HSSP; P00560; 10PG.
InterPro; IPR001576; PGK.
Pfam; PF00162; PGK; 1.
                                                                                                                                                                                                                                                                                                                                              5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                          QKAGGF 187
                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     1 EKAGGF 6
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P50310;
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SEQUENCE
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SEQUENCE
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PGG CRIGR

ID PGG CRIGR

DT 01-0C

DT 01-0C

DT 01-0C

DT 01-0C

CC Crice

OX CRICE

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90.6%; Score 29; DB 1; Length 416;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Primary structure of 3-phosphoglycerate kinase from horse muscle. II. Amino acid sequence of cyanogen bromide peptides CB1-CB4 and CB6-CB14, sequence of methionine-containing regions, and complete sequence of the enzyme."; J. Biol. Chem. 256:10293-10305(1981).
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JOIN DOWAIN 1 AND 2.
GLOBULAR DOWAIN 2.
GLOBULAR DOWAIN 1.
ASSOCIATED WITH GLOBULAR DOWAIN 1.
ADP-ATP ALPHA-PHOSPHATE.
ADP-ATP ADENINE RING.
ADP-ATP ADENINE RING.
ADP-ATP ADENINE RING.
RIBOSE OF ADP-ATP.
                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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InterPro; IPR001576; PGK.
PRAM; PR00157. PGK.
PRINTS; PR00477; PHGLYCKINASE.
PROSITE; PS00111; PGLYCERATE KINASE; 1.

MOD RES A Cetylation, Glycolysis; 3D-structure.

MOD RES (A CONTINE TO CONTINE 
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Pred. No. 70;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A4B926A6FE0B0FDA CRC64;
                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-CUL-2003 (Rel. 42, Last annotation update)
Phosphoglycerate kinase (EC 2.7.2.3).
416 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=82030789; PubMed=7287713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=79199779; PubMed=450128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44471 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.6%;
83.3%;
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Matches 5; Conservative
          STANDARD;
                                                                                                                                                                                                                                                                                                                                                     Equus caballus (Horse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 QKAGGF 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    416 AA;
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VARIANT CHRONIC HEMOLYTIC ANEMIA/MENTAL RETARDATION VAL-163, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. 255:6421-6423(1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hemoglobin 4:601-609(1980).
                                                                                                 Blood 84:898-903(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT MUNCHEN ASN-267.
                                                                                      Amiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kinase.
      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Phosphoglycerate kinase 1 (EC 2.7.2.3) (Primer recognition protein 2)
                                                                                                                                                                                                                                             SEQUENCE OF 1-416 FROM N.A.
MEDLINE=86016816; PubMed=2995995;
Michelson A.M., Blarke C.C., Farans S.T., Orkin S.H.;
Michelson A.M., phaske C.C., Farans S.T., orkin S.H.;
Michelson A.M., phosphoglycerate kinase gene and the intronmediated evolution and dispersal of the nucleotide-binding domain.";
Proc. Natl. Acad. Sci. U.S.A. 82:6965-6969(1985).
                                                                                                                                                                                       Michelson A.M., Markham A.F., Orkin S.H.;
"Isolation and DNA sequence of a full-length cDNA clone for human X
chromosome-encoded phosphoglycerate kinase.";
Proc. Natl. Acad. Sci. U.S.A. 80:472-476(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-20 FROM N.A. MEDLINE=88155507; PubMed=6099325; Singer-Sam J., Keith D.H., Tani K., Simmer R.L., Shively L., Lindsay S., Yoshida A., Riggs A.D.; "Sequence of the promoter region of the gene for human X-linked 3-phosphoglycerate kinase].";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-13 FROM N.A. MEDLINE=90049205; PubMed=2814502; Pfeifer G.P., Steigerwald S.D., Mueller P.R., Wold B., Riggs A.D., "Genomic sequencing and methylation analysis by ligation mediated
                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Hematologically important mutations: molecular abnormalities of phosphoglycerate kinase.";
Blood Cells Mol. Dis. 22:265-267(1996).
                                                                                                                                                                                                                                                                                                                                         TISSUE=Exythrocyte,
MEDLINE=80227775, PubMed=7391027;
Huang I.-Y., Welch C.D., Yoshida A.;
"Complete amino acid sequence of human phosphoglycerate kinase.
Cyanogen bromide peptides and complete amino acid sequence.";
J. Biol. Chem. 255:6412-6420(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT CHRONIC HEMOLYTIC ANEMIA LYS-190 DEL.
MEDLINE=96230923; PubMed=8673469;
Yoshida A., Twele T.W., Dave V., Beutler E.;
"Molecular abnormality of a phosphoglycerate kinase variant
                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Placenta;
MEDLINE=90216667; PubMed=2324090;
Jindal H.K., Phewanatha J.K.;
Functional identity of a primer recognition protein as phosphoglycerate kinase.";
J. Biol. Chem. 265:6540-6543(1990).
   417 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PGK-Alabama) ";
Blood Cells Mol. Dis. 21:179-181(1995)
[9]
   PRT;
                                                                                                                                                                           MEDLINE=83169680; PubMed=6188151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97230014; PubMed=9075577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 246:810-813(1989)
  STANDARD;
                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 32:409-417(1984)
                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                           PARTIAL SEQUENCE,
                                                                                 OR PGKA.
  HUMAN
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                                                                                                                                                                                                                                                                                                                               SEQUENCE
            P00558;
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VARIANT RHABDOMYOLYSIS ASN-314.
MEDLINE=94318968; PubMed=8043870;
Cohen-Solai M., Valentin C., Plassa F., Guillemin G., Danze F.,
Jaisson F., Rosa R.,
"Identification of new mutations in two phosphoglycerate kinase (PGK)
variants expressing different clinical syndromes: PGK Creteil and PGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A phosphoglycerate kinase mutant (PGK Herlev; D285V) in a Danish patient with isolated chronic hemolytic anemia: mechanism of mutation and structure-function relationships.";
Hum. Mutat. 12:280-287(1998).
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96201344, PubMed=8615693, Ookawara T., Dave V., Willems P., Martin J.J., de Barsy T., Matthys E., Yoshida A., "Retarded and aberrant splicings caused by single exon mutation in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=80227776, PubMed=7391028,
Fujii H., Krietsch W.K.G., Yoshida A.;
"A single amino acid substitution (Asp leads to Asn) in a
Phosphoglycerate kinase variant (PGK Munchen) associated with enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT MUNCHEN ASN-267, AND VARIANT ASN-351.
MEDLINE=81069227; Pubmed=7440217;
Huang I.-Y., Fujii H., Yoshida A.;
"Structure and function of normal and variant human phosphoglycerate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT CHRONIC NONSPHEROCYTIC HEMOLYTIC ANEMIA MET-265.
MEDINE=81223926, PubMed=6941312,
Fulii H., Chen S., H., Akatsuka J., Miwa S., Yoshida A.,
"Use of cultured lymphoblastoid cells for the study of abnormal
enzymes: molecular abnormality of a phosphoglycerate kinase variant
associated with hemolytic anemia.",
Proc. Natl. Acad. Sci. U.S.A. 78:2587-2590(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT CONGENITAL NONSPHEROCYTIC ANEMIA PRO-87.
MEDLINE=91159642; PubMed=2001457;
Maeda M., Yoshida A.;
Molecular defect of a phosphoglycerate kinase variant (PGK-Matsue)
associated with hemolytic anemia: Leu-->Pro substitution caused by
T/A-->C/G transition in exon 3.";
Blood 77:1348-1352(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92190498; PubMed=1547346; Fujii H., Kanno H., Hirono A., Shiomura T., Miwa S.; Fujii H., Kanno H., Hirono A., Shiomura T., Miwa S.; "A single amino acid substitution (157 Gly-->Val) in a phosphoglycerate kinase variant (PGK Shizuoka) associated with chronic hemolysis and myoglobinuria."; Blood 79:1582-1585(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT CHRONIC HEMOLYTIC ANEMIA ARG-315.
MEDLINE=92265933; PubMed=1586722;
Maeda M., Bawle E.V., Kulkarni R., Beutler E., Yoshida A.;
"Molecular abnormalities of a phosphoglycerate kinase variant
generated by spontaneous mutation.";
Hlood 79:2759-2762(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98415729; PubMed=9744480;
Valentin C., Birgens H., Craescu C.T., Broedum-Nielsen K.,
Cohen-Solal M.;
                                                                                                                                                                                                                                                                                                                                                                       VARIANT CHRONIC HEMOLYTIC ANEMIA ALA-251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphoglycerate kinase variant.";
Arch. Biochem. Biophys. 327:35-40(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT CHRONIC HEMOLYTIC ANEMIA VAL-284
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KRE2 OR MNT1.
Candida albicans (Yeast).
                                                                         SEQUENCE FROM N.A.
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                                                   NCBI_TaxID=5476;
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P53966;
                                                                                                                            GOW N.A.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Golgi stack
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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KTR5_YEAST
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                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  WEDLINE-8105487; PubMed-6933565;
WEDLINE-8105487; PubMed-6933565;
WEDLINE-81054887; PubMed-6933565;
WEDLINE-81054887; PubMed-6933565;
Wedli H., Yoshida A.;
Fudli H., Yoshida A.;
Fudli H., Yoshida A.;
Fudli H., Sanda B.;
Wholecular abnormality of phosphoglycerate kinase-Uppsala associated
with chronic nonspherocytic hemolytic anemia.";
Fuc. Natl. Acad. Sci. U.S. A. 77:5461-5465[1980].

L. FUNCTION: In addition to its role as a glycolytic enzyme, it seems that PGK-1 acts as a polymerase alpha cofactor protein
C. --- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-phospho-D-glyceroyl phosphate.
C. --- PATHWAY: Second phase of glycolysis; second step.
C. --- PATHWAY: Second phase of glycolysis; second step.
C. --- DISEASE: Defects in PGKL are generally associated with chronic hemolytic anemia [MIM:311800]; although it can be accompanied by either mental retardation or muscular disease (rhabdomyolysis).
C. --- SIMILARITY: Belongs to the phosphoglycerate kinase family.
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glycolipid 2-alpha-mannosyltransferase (EC 2.4.1.131) (Alpha-1,2-mannosyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00162; PGK; 1.
PRINTS; PR00477; PHGINCKINASE.
PROSITE; PS00111; PGINCERATE KINASE; 1.
Transferase; Kinase; Multigene family; Glycolysis; Acetylation; Disease mutation; Polymorphism; Hereditary hemolytic anemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.6%; Score 29; DB 1; Length 417; 83.3%; Pred. No. 71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GK, P00558; -.
MIM, 311800; -.
GO; 0004618; F:phosphoglycerate kinase activity; TAS.
InterPro; IPR001576; PGK.
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                                                                                                                                                                                                                                                                                                                               EMBL; V00572; CAA23835.1; -.
EMBL; M11958; AAA60079.1; -.
EMBL; M11959; AAA60079.1; JOINED.
EMBL; M11959; AAA60079.1; JOINED.
EMBL; M11960; AAA60079.1; JOINED.
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AAA60079.1; JOINED.
AAA60079.1; JOINED.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                  M11961;
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Q00310;
01-NOV-1997 (
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EMBL;
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KRE2 CANAL
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ID AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PATHWAY: Glycosylation.
-!- SUBCELLULAR LOCATION: Type II membrane protein. Golgi (Potential).
-!- SIMILARITY: Belongs to the glycosyltransferase family 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL) .
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                           "Molecular analysis of CaMntlp, a mannosyl transferase important for adhesion and virulence of Candida albicans.";
Proc. Natl. Acad. Sci. U.S.A. 95:7670-7675(1998).
-!- FUNCTION: REQUIRED FOR THE ATTACHMENT OF THE THIRD MANNOSE
RESIDUE OF O-LINKED SACCHARIDES (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: Transfers an alpha-D-mannosyl residue from GDP-mannose into lipid-linked oligosaccharide, forming an alpha-
1,2-D-mannosyl-D-mannose linkage.
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Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002685; Glyco trans 15.
Pfam; PF01793; Glyco transf 15; I.
Transferase; Glycosyltransferase; Transmembrane; Signal-anchor;
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S
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Andre B., Iraqui Houssaini I., Urrestarazu L.A., Vissers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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Duesterhoeft A., Floeth M., Fritz C., Heuss-Neitzel D., Hilbert H., Moestl D. 5.
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LUMENAL (POTENTIAL).
NUCLEOPHILE (POTENTIAL).
BRACIFAE9010B763 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1093 (Rel. 41, Last annotation update)
Probable mannosyltransferase KTRS (EC 2.4.1.131).
KTRS OR YNL029C OR N2755.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 522 AA
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                                                                                                                                                                                                              MEDLINE=98301633; PubMed=9636208;
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318 318 N
431 AA; 50004 MW;
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28
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                     631 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330 EKAGGY 335
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EKAGGF 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116
                                                                                    Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA13 RAT
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                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                         CATALYTIC ACTIVITY: Transfers an alpha-D-mannosyl residue from GDP-mannose into lipid-linked oligosaccharide, forming an alpha-mannosyl-D-mannose linkage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
                                MEDINE-97245297, PubMed-9090056;
Lussier M., Sdicu A.-M., Winnett E., Vo D.H., Sheraton J.,
Lussier M., Sdicu R.K., Bussey H.;
Completion of the Saccharomyces cerevisiae genome sequence allows identification of KTR5, KTR6 and MFTR7 and definition of the nine-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STEM REGION (CARACTER (BY SIMILARITY).
NUCLEOPHILE (POTENTIAL).
(CARACTER (CARACTER).) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycosyltransferase; Transmembrane; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Type II membrane protein (Probable) -!- SIMILARITY: Belongs to the glycosyltransferase family 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                        EMBL; Z71305; CAA95891.1; -.
PIR; S62941; S6294.
Germonline; 143036; -.
SGD; S000474; KTR5
GO; GO:0007047; Preel wall organization and biogenesis; IMP InterPro; IPR002685; Glyco_trans 15.
Pfam; PF01793; Glyco_trans 15.
                                                                                                   membered KRE2/MNT1 mannosyltransferase gene family in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 29; DB 1; Length 522;
Pred. No. 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LUMENAL (POTENTIAL).
STEM REGION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -LINKED (GLCNAC. . .) (POSTSD3F09D4110 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                           Yeast 13:267-274(1997).
-!- FUNCTION: POSSIBLE GLYCOSYLTRANSFERASE.
-!- CATALYTIC ACTIVITY: Transfers an alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61727 MW;
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37
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38
83
363
86
522 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase;
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01-NOV-1995
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                                                                                                                    organism."
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P44236;
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CARBOHYD
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                                                                                                                                                                          "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94114571; PubMed=8286415; Glumoff V., Maekelae J.K., Vuorio E.; Cloning of cDNA for rat pro alpha 1(III) collagen mRNA. Different expression patterns of type I and type III collagen and fibronectin genes in experimental granulation tissue."; Biophys. Acta 1217:41-48(1994).
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C. Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen M.S.M., Geofface C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 308-482 FROM N.A.
MEDLINE=88296083; PubMed=2456904;
Frankel F.R., Hsu C.-Y.J., Meyers J.C., Lin E., Lyttle C.R.,
Komm B., Mohn K.;
"Regulation of alpha 2(I), alpha 1(III), and alpha 2(V) collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 73-636 FROM N.A. STRAIN-Sprague-Dawley; TISSUE-Fibroblast; ... Wurtz T., Ellerstroem C., Lundmark C., Christersson C.; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34E234C986406DE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 29; DB 1;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P13941; O70604;
01-JAN-1990 (Rel. 13, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
06-CCT-2001 (Rel. 40, Last annotation update)
Collagen alpha 1(III) chain (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   636 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U32827; AAC23167.1; -.
PIR; C64034; C64034.
TIGR; H11514; -,
Hypothetical protein; Transme
                                                                                                                                                                                                                       Science 269:496-512(1995).
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   mRNAs by estradiol in the immature rat uterus.";
DNA 7:347-354(1988).
-!- FUNCTION: Collagen type III occurs in most soft connective tissues
along with type I collagen.
-!- SUBUNIT: Trimers of identical alpha 1(III) chains. The chains are
linked to each other by interchain disulfide bonds. Trimers are
also cross-linked via hydroxylysines.
-!- PTM: Prolines at the third position of the tripeptide repeating
-unit (G-X-Y) are hydroxylated in some or all of the chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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ProDom; PD002078; Fib_collagen_C; 1.
SMART; SM00038; COLFI; 1.
PROSITE; PS01208; WWFC 1; PARTIAL.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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NONHELICAL REGION (C-TERMINAL).

INTERCHAIN (BY SIMILARITY).

INTERCHAIN (BY SIMILARITY).

N -> D (IN REF. 2).

A -> G (IN REF. 2).

M, 61A48159F01D01EE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COLLAGEN ALPHA 1 (III) CHAIN. CARBOXYL-TERMINAL PROPEPTIDE.
estradiol in the immature rat uterus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, X70369; CAA49832.1; ---
EMBL, AJ00539; CAA6510.1; ---
EMBL, MA1354; AAA40942.1; ---
PIR; S41067; S41067.
InterPro; IPR008161; Clg helix.
InterPro; IPR008161; Collagen.
InterPro; IPR008169; Fibrinogen_C.
InterPro; IPR002181; Fibrinogen_C.
Pfam; PF014910; COLFI; 1.
Pfam; PF014910; COLFI; 1.
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NON TER 1
CHAIN <1 375
PROPEP 376 636
DOMAIN <1 368
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369
340
429
636 AA;
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hes 5; Conserv
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Search completed: September 18, 2004, 04:26:19 Job time : 6.47059 secs

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us-10-615-959-39.rspt

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Q7v1t3 prochloroco
Q811g9 bacillus an
Q80480 streptococo
Q7vgh7 helicobacte
Q888d3 pseudomonas
Q9n6u4 homo sapien
Q9x087 thermotoga
Q9x087 thermotoga
Q9x097 thermotoga
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Q8les8 arabidopsis
Q84k40 arabidopsis
Q8a9g0 caulobacter
Q818d7 bacillus ce
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Q8abw1 bacteroides
                                                                                                                                 September 18, 2004, 04:00:08 ; Search time 21.2941 Seconds (without alignments) 88.903 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                 1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                       OM protein - protein search, using sw model
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Q8DV80
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Q9A9G0
Q818D7
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Gapop 10.0 , Gapext 0.5
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Q8ABW1
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_bacteriap:*
sp_archeap:*
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sp_phage:*
sp_plant:*
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sp_bacteria:*
sp_fungi:*
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seq length: 200000000
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MEDLINE=2285598; PubMed=12917642;
Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
Rocap G., Larimer F.W., Londen M., Hauser L., Hess W.R.,
Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
Webb B.A., Zinser E.R., Chisholm S.W.;
"Genome divergence in two Prochlorococcus ecotypes reflects oceanic
                                                                                                                                         Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
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EMBL; BX572092; CAE19231.1; -.

Hypothetical protein; Complete proteome.

SRQUENCE 182 AA; 20358 MW; 24C6151DC9065CE6 CRC64;
                                              01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
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                                   182 AA
                                   PRT;
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                      Prochlorococcus.
NCBI_TaxID=59919;
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RESULT 2 Q81LQ9

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Les 6; Conservative
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                                                                                                                                                                     Complete proteome.
SEQUENCE 225 AA;
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Matches
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Q888D3
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SERAILE-MAIS / Arcc 700610 / Serotype C;
STRAILE-MAIS / Arcc 700610 / Serotype C;
MEDLINE-22295063; PubMed=12397186;
Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Prineaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti J.J.;
"Genome sequence of Streptococcus mutans UAIS9, a carlogenic dental
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
Read T.D., Peterson S.N., Tourasse N., Eisen J.A., Gill S.R.,
Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
Rolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.W., Gwinn M.,
DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
Berty K.J., Plaut R.D., Wolff A.M., Warkins K.L., Nierman W.C.,
Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria.";
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                    COMEA ÔR BA4553.
Bacillus anthracis (strain Ames).
Bacteria; Firmicutes; Bacillales; Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 AA; 22368 MW; 8A8C00E89B5CC3E8 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
EMBL; ASD14906; AANS8359.1; -.
                                                (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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        198 AA
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GO; GO:0003677; F:DNA binding; IEA.
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TIGREAMS; TIGR00426; TIGR00426; 1.
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EMBL; AE017038; AAP28261.1; -.
TIGR; BA4553; -.
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InterPro; IPR000445; HhH.
InterPro; IPR003583; HHH_1.
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Best Local Similarity luv.
6, Conservative
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        PRELIMINARY;
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NCBI_TaxID=1309;
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                                 Q81LQ9;
01-JUN-2003
01-JUN-2003
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EMBL; AE017148; AAAP77941.1; -
Hydrolase; Complete procheme.
SEQUENCE 279 AA; 31175 WW; F6D4AEAZ0DFDEEERC CRC64;
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter hepaticus.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=32025;
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Relaxase/mobilization nuclease domain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Pructose-1,6-biphosphatase (EC 3.1.3.11).
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro: IPR004509; ComEA HHH.
InterPro: IPR004583; HHH.
InterPro: IPR003583; HHH_1.
Ffan; PF00633; HHH; 2.
SWART; SN00278; HHH1; 2.
TIGREAMS; TIGR00426; TIGR00426; 1.
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SEQUENCE FROM N.A.
STRAIN=ATCC 51449 / 3B1;
MEDLINE=22709201; PubMed=12810954;
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

B Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

R SUD (20.0019781; C.collagen; I.E.

GO; GO:0005501; F:extracellular matrix structural constituent; IEA.

R GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

InterPro; IPR001816; Fibrinogen C.

R InterPro; IPR001007; VWF_C.

R InterPro; IPR01007; VWF_C.

R Pfam; PF01410; COLFI; 1.

R ProDom; P0002078; Fib_collagen, C; 1.

R ProDom; P0002078; Fib_collagen_C; 1.

R SMRAT; SM00038; COLFI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D., Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M., Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S., Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T., White O., Fraser C., Collmer A.; "Complete sequence of Pseudomonas syringae."; Submitted (WAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AED16859; AAO54622.1; -.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant).
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
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Pfam; PF03423; Relaxase; 1.
Complete proteome:
SEQUENCE 805 AA; 92502 MW;
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Best Local Similarity 100..
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Matches 6; Conserv
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SEQUENCE
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QBN6U4;
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Q9X087
ID Q9X01
AC Q9X01
DT 01-NC
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STRAIN=MSB8 / DSM 3109;

X MEDLINE=99287316; PubMed=10360571;

A Nelson K.E.; Clayton R.A.; Gill S.R., Gwinn M.L., Dodson R.J.,

A Haft D.H., Hickey E.K., Pratt M.S., Pillips C.A.; Richardson D.,

Stewart A.M., Cottcon M.D., Pratt M.S., Pillips C.A.; Richardson D.,

Heidelberg J., Sutton G.G., Pleischmann R.D., Eisen J.A., White O.,

A Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Bydonce for lateral gene transfer between Archaea and Bacteria from Inquire 399:323-329 (1999).

I Mature 399:323-329 (1999).

R EMBL; ARONOT761; AAD36071.1; -.
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Fox B.A., Baik D.J.;

Flox B.A., Baik D.J.;

Phosphate synthetase II in Toxoplasma gondii.";

Int. J. Parasitol. 0:0-0(2002).

EMBL; AV05630; AAL27793.2; -..

GO, GO:0005737; C:0xtoplasm; IEA.

GO; GO:0005737; F:ATP binding; IEA.

GO; GO:0016894; F:ATP binding; IEA.

GO; GO:0016894; F:Iigase activity; IEA.

GO; GO:0016894; F:Iigase activity; IEA.

GO; GO:0016897; P:nitrogen metabolism; IEA.

GO; GO:0016897; P:nitrogen metabolism; IEA.

GO; GO:0018866; P:pyrimidine base biosynthesis; IEA.
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Bukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
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                                                                                            Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
NCBI_TaxID=2336;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Complete protecome.
SEQUENCE 1289 AA; 148491 MW; 82E5081AD98ADCAA CRC64;
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Carbamoyl phosphate synthetase II (EC 6.3.5.5).
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InterPro; IPR006275; CarA_L glu.
InterPro; IPR006274; CarA_synth_small.
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                             Hypothetical protein TM0992.
TM0992.
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Nature 415:926-929(2002).
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hes 6; Conservative
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Q8T9L7
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STRAIN=VPI-5482 / ATCC 29148;
STRAIN=VPI-5482 / ATCC 29148;
STRAIN=VPI-5580858; PubMed=12663928;
Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
Science 299:2074-2076(2003).
EMBL; AY171301; AA045335.1; --
EMBL; AY171301; AA045335.1; --
EMBL; AY171301; AA045335.1; --
EMBL; AY171301; AA045335.1; --
Hypochhetical protein; Plasmid; Complete proteome.
SEQUENCE 127 AA; 13842 MW; CD375C8A72D939BB CRC64;
                                 01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 22, Last annotation update)
01-0CT-2000 (TremBlrel. 22, Last annotation update)
04066H10.8 protein (0J174_005.3 protein).
0722a sativa (Rice).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Bacteroidaceae; Bacteroides.
NCBI_TaxID=818;
                                                                                                                                                                                                                                                                               STRAIN=cv. Nipponbare;
Saski T., Matenmoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
-clone:P0406H10.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
SABAKI T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
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B3.3%; Pred. No. 1.9e+02;
Live 1; Mismatches 0; Indels
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Submitted (JĀN-2001) to the EMBL/GenBank/DDBJ databases
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101 AA; 10946 MW; 2358947F354AD8D3 CRC64;
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Bacteroides thetaiotaomicron.
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Best Local Similarity 83.5
PRELIMINARY;
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SEQUENCE 101 AP
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091.GG6;
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Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F., Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F., Dandson R.J., Umayam L., Brinkac L.M., Beanan M.J., Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R., Nelson W.C., Ayodeji B., Kraul M., Shetry J., Malek J., Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.; "The Brucella suis genome reveals fundamental similarities between animal and plant pathogens and symbionts.";

Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).

EMBL, AR01922; --.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 32; DB 5; Length 1687; 100.0%; Pred. No. 7.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.6%; Score 29; DB 16; Length 46; 83.3%; Pred. No. 86; cive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Ligase.
SEQUENCE 1687 AA; 185865 MW; FA9979489DCCC509 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Complete proteome. SEQUENCE 46 AA; 4696 MW; 3AAB1BE91BD0F138 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
              InterPro; IPR00549; CPase_L D2.
InterPro; IPR005489; CPase_L D2.
InterPro; IPR005481; CPase_L D3.
InterPro; IPR005481; CPase_L D3.
InterPro; IPR001317; CP synthGATase.
InterPro; IPR00297; CP synthSmall.
InterPro; IPR00299; CPSase_L D3 i.
Pfam; PF02786; CPSase_L D2 i.
Pfam; PF02786; CPSase_L D3; 1.
PRIWTS; PR00099; CPSATRASEII.
PRIWTS; PR00099; CPSATRASEII.
PRIWTS; PR00099; CPSATRASEII.
PRIWTS; PR00099; CPSATRASEII.
TIGRRAMS; TIGR01369; CPSASEII.
TIGRRAMS; TIGR01369; CPSASEII.
PROSITE; PS00866; CPSASE_I; I.
PROSITE; PS00867; CPSASE_I; I.
      InterPro; IPR005483; CPase_L.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity luv...
6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       863 EKAGGF 868
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RESULT 9 Q8G360

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RESULT 10 Q9LGG6

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154 ERAGGF 159

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O1-OCT-2002 (TrEMBLrel. 22, Created)
O1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
O1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
Hypotherical protein.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TAXID=3702;
                                                                                                                                                                                                                                                Coombs J.T., Franco C.M.M., Loria R.;
"Complete sequencing and analysis of pEN2701, a novel 13kb plasmid
from an endophytic Streptomyces sp.";
Plasmid 0:0-0(202).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
"Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=211464;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.6%; Score 29; DB 10; Length 178; 83.3%; Pred. No. 3.48+02; 1ve 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                           90.6%; Score 29; DB 2; Length 152; 83.3%; Pred. No. 2.9e+02; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Full-Length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AX085254; AM62486.1; -.
Hypochetical protein.
SEQUENCE 178 AA; 20047 MW; 3A0D3BBAA314EF24 CRC64;
                                                                                                                                                                                                                                                                                                              EMBL, AF533985, AAN76280.1; -.
GO: GO46821; C:extrachronosomal DNA; IEA.
Hypothetical protein; Plasmid: BR21C8DA9FC9D56 CRC64; SEQUENCE 152 AA; 15024 NW; 1EB21C8DA9FC9D56 CRC64;
                                                                              Last sequence update)
Last annotation update)
                                   152 AA
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                                                               23, Created)
23, Last seque
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Query Match
Best Local Similarity 83.33,
Lag 5; Conservative
                                PRELIMINARY;
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Matches 5; Conservative
                                                              (TrEMBLrel.
                                                                            (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                     Hypothetical protein.
Streptomyces sp. EN27.
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                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                         Plasmid pEN2701
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                                                                                           01-JUN-2003
                                                            01-MAR-2003
01-MAR-2003
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RESULT 12
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QBLES8
              DAGGE6
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SEQUENCE FROM N.A.

Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,

Yamada K., Chan M.M., Tang C., Toziluni M., Wong C., Wu H.C.,

Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,

Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,

Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,

Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
Yamada C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
Nguyen M., Palm C.J., Sakurai T., Sacou M., Seki M., Shinn P.,
Theologis A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=ATCC 19089 / CB15;
MEDLINE=21173699; PubMed=11259647;
Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potcocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
                                                                                                                                                                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                           Theologis A.;
"Arabidopsis Full Length cDNA Clones.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Arabidopsis Full Length cDNA Clones.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 178 AA; 20077 MW; 26614BA6CF64EF24 CRC64;
                                                                      01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Mypothetical protein CC1028.
CC1028.
Caulobacter crescentus.
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                                       178 AA
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                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
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                                       PRT;
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                                     PRELIMINARY;
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                                                                                                                          Hypothetical protein. AT4G30820.
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154 ERAGGF 159
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                NCBI_TaxID=3702;
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01-JUN-2001 (
01-JUN-2003 (
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RESULT 14
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RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RI "Complete genome sequence of Caulobacter crescentus.";
R. Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AR005780; AAK23012.1; -.
DR PIR; H87376; H87376.
DR TIGR; CC1028; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 187 AA; 19496 MW; 9C2B20F466B2D566 CRC64;
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-Db 126 ERAGGF 131 Search completed: Sentember 18, 2004, 04:29

1 EKAGGF 6

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Query Match
90.6%; Score 29; DB 16; Length 187;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels

Search completed: September 18, 2004, 04:29:34 Job time: 25.2941 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

sw model using OM protein - protein search,

Run on:

September 18, 2004, 03:47:39; Search time 42.8235 Seconds (without alignments) 52.784 Million cell updates/sec

US-10-615-959-40 Title: Perfect score:

1 IGGEKAGG 8 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

geneseqp1980s:\*
geneseqp1990s:\*
geneseqp2000s:\*
geneseqp2001s:\* A Geneseq 29Jan04:\* 1: geneseqp1980c.\* geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:\*

Aay29125 Amino aci		Aay68425 Type III		Aay82167 Type II a	Aab51275 Collagen					Abb09628 Amino aci						Abu19644 Proteîn e	Aar88469 Feline in		
AAY29125	ABM70142	AAY68425	AAY68436	AAY82167	AAB51275	AAR71704	AAY96125	AAE16478	ABB80736	ABB09628	AAY20721	AAG34474	ABP70959	ABG08457	ABB64897	ABU19644	AAR88469	AAE02534	AAE02533
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674	481	11	11	11	11	1078	1078	1078	1078	1078	128	162	320	357	601	691	1464	1466	1466
90.5	88.1	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	83,3	83.3	83.3		83.3		83.3	83.3	83.3
38	37	36	36	36	36	36	36	36	36	36	32	32	35	32	35	35		32	
26	27	28	29	30	31	32		34	35	36		38	39	40	41	42	43	44	45

### ALIGNMENTS

AAB61740 standard; peptide; 8 AA. 20-APR-2001 (first entry) AAB61740; RESULT 1 AAB61740 

Human type III collagen carboxy-telopeptide fragment.

Type II collagen; immunoassay; cartilage; telopeptide; human; type III collagen.

Synthetic. Homo sapiens.

WO200079284-A1.

99US-00335098. 99US-0141574P. 99US-0142274P. 99WO-US029357. 17-JUN-1999; 29-JUN-1999; 02-JUL-1999; 07-JUL-1999; 10-DEC-1999; 28-DEC-2000.

99US-0142675P. (WASH-) WASHINGTON RES FOUND. 30-AUG-1999;

Eyre DR;

WPI; 2001-146859/15.

Assay for detecting cross-linked telopeptide analytes indicative of type II collagen resorption in vivo in a body fluid sample, comprises contacting the sample with an antibody which binds to the analyte.

Disclosure; Page 15; 34pp; English.

The invention relates to immunoassays for measuring type II collagen (cartilage) resorption in vivo. The method of analysing a body fluid sample for the presence of an analyte indicative of a physiological condition, involves contacting the body fluid sample with an antibody (Ab) which binds to the analyte, detecting binding of Ab in the body fluid sample, and correlating any detected binding to the physiological condition. The analysis is useful for measuring type II collagen (cartilage) resorption in vivo, for distinguishing between resorption of

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assay for detecting cross-linked telopeptide analytes indicative of type II collagen resorption in vivo in a body fluid sample, comprises contacting the sample with an antibody which binds to the analyte.
non-mineralized and mineralized cartilage, and for measuring total cartilage resorption in vivo. The present sequence represents a linear synthetic peptide based on the carboxy-terminal telopeptide sequence of human collagen type III
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Pred. No. 1.4e+06;
                                                                           100.0%; Score 42; DB 4; Length 8; larity 100.0%; Pred. No. 1.4e+06; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                         Human type III collagen carboxy-telopeptide fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 15; 34pp; English
                                                                                                                                                                                             AAB61741 standard; peptide; 9 AA.
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99US-0142274P.
99US-0142675P.
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                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human collagen type III
                                                                  Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                     IGGEKAGG
                                                                                                                                          IGGEKAGG
                                                                                                                                                                                                                                                                                          type III collagen.
                                                                                                                                                                                                                                                                                                                                              WO200079284-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9 AA;
                                                        Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                               Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assay for detecting cross-linked telopeptide analytes indicative of type II collagen resorption in vivo in a body fluid sample, comprises contacting the sample with an antibody which binds to the analyte.
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                                                                                                                                                                                                                                                                                                                                                   Human type III collagen carboxy-telopeptide fragment.
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                                                                                                                                                                                            AAB61742 standard; peptide; 11 AA.
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99US-0142274P.
99US-0142675P.
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Best Local Similarity
                                                       IGGEKAGG
1 IGGEKAGG
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Query Match
Best Local Similarity
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                                   telopeptide alpha
                                                                         WO2003068919-A2
                                                                                                                                                                            Hellerstein MK;
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                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                (cartilage) resorption in vivo. The method of analysing a body fluid sample for the presence of an analyte indicative of a physiological condition, involves contacting the body fluid sample with an antibody fluid sample, and correlating any detecting binding of Ab in the body fluid sample, and correlating any detected binding to the physiological condition. The analysis is useful for measuring type II collagen (cartilage) resorption in vivo, for distinguishing between resorption of non-mineralized and mineralized cartilage, and for measuring total cartilage resorption in vivo. The present sequence represents a linear synthetic peptide based on the carboxy-terminal telopeptide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; therapy; osteoporosis; left-ventricular hypertrophy; scleroderma;
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                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to immunoassays for measuring type II collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
                                                                              Type II collagen; immunoassay; cartilage; telopeptide; human; type III collagen.
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                                                           Human type III collagen carboxy-telopeptide fragment.
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AAB61743 standard, peptide, 12 AA.
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                                                                                                                                                                                                      99US-00335098.
99US-0141574P.
99US-0142274P.
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Best Local Similarity
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                                                                                                                                          WO200079284-A1
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                                                                                                                       Homo sapiens.
                                                                                                                                                                                  10-DEC-1999;
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                    AAB61743
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   fibrosis; mellitus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determining rate of biosynthesis or breakdown of inaccessible biological molecules, useful e.g. for diagnosis or monitoring treatment, by administering labeled precursor.
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liver cirrhosis; congestive heart failure; multiple sclerosis; fibrosi coal-miner's pneumoconiosis; muscle-wasting syndrome; diabetes mellitu rheumatoid arthritis; Alzheimer's disease; muscular dystrophy; cancer;
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Misc-difference 17
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RESULT

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AAR92061-R92069 represent N-terminal and C-terminal peptides of the recombinant human collagen polypeptides of the invention. This sequence represents the C-terminal peptide of a recombinant human alpha1(III) collagen of the invention. The recombinant pro-collagen of the invention recombinant pro-collagen of the invention comprises a natural collagen polypeptide chain, a pro-peptide, and a non-natural site-specific proteolytic agent recognition site between the collagen and pro-peptide. The recombinant pro-collagens are used to produce collagens which can be used in tissue and cell cultures. The collagens can also be used as biocompatible materials such as arrificial skin, sutures, haemostatic sponges or tissue augmentation compositions for use in humans. The pro-peptide increases the yield of secreted pro-collagen. The increase in yield of the pro-collagen, as compared to cells expressing the collagen chains alone, is at least 1000%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant production of collagen - by expressing a pro-peptide-collagen sequence and cleaving at an intermediate proteolytic recognition site.
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/note= "any amino acid except Glu"
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Best Local Similarity 100.
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                                                                                                                                                                      Misc-difference 23
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                 Misc-difference 18
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The invention relates to a method of determining the rate of biosynthesis or breakdown of at least one inaccessible biological molecule in a subject. The method is useful for dagnosis or monitoring and treatment of diseases associated with an altered rate of biosynthesis/breakdown of an isotopically labelled precursor molecule, specifically osteoporosis; left-ventricular hypertrophy; liver cirrhosis or fibrosis; congestive heart failure; scleroderma; coal-miner's pneumoconiosis; congestive fibrosis; Alzheimer's disease; multiple sclerodis; rheumatoid arthritis; diabetes mellitus; muscle-wasting syndromes; muscular dystrophy; athletic training and cancer. The method is also useful for screening candidate gene or protein targets, phenotypic/human validation studies on potential disease. The present sequence is human collagen type I cross-linked carboxy terminal peptide (ICTP). This sequence is used to illustrate the
                                                                                                                                                   Human; therapy; osteoporosis; left-ventricular hypertrophy; scleroderma; liver cirrhosis; congestive heart fallure; multiple sclerosis; fibrosis; coal-miner's pneumoconfosis; muscle-wasting syndrome; diabetes mellitus; rheumatoid arthritis; Alzheimer's disease; muscular dystrophy; cancer; collagen type I cross-linked carboxy-terminal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining rate of biosynthesis or breakdown of inaccessible biological molecules, useful e.g. for diagnosis or monitoring treatment, by administering labeled precursor.
                                                                                                                 Human collagen type I cross-linked C-terminal peptide, PIIICP(alphal).
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               AAE38640 standard; protein; 262 AA.
                                                                                                                                                                                                                                                                                                                                                                            12-FEB-2003; 2003WO-US004183
                                                                                                                                                                                                                                                                                                                                                                                                                  12-FEB-2002; 2002US-0356008P
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                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-689661/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 262 AA;
                                                                                                                                                                                                                                                                                                        WO2003068919-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hellerstein MK;
                                                                                                                                                                                                                                                                        sapiens
                                                                                      04-DEC-2003
                                                                                                                                                                                                                                                                                                                                            21-AUG-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY07375;
                                                    AAE38640;
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                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
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4AE38640
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Daviet L;
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                                                                                                                                                                        (HYBR-) HYBRIGENICS.
                                                                                                                                                                                                                          WPI; 2003-103412/09.
                                                                                                                                                                                                                                                                                                      obesity or diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IGGEKAGG 8
                                                                                                                                                                                                                                      N-PSDB; ACA57357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 293 AA;
                                                                  WO200286122-A2
                                           Homo sapiens
                                                                                            31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-DEC-2001
                                                                                                                                                                                                Legrain P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU23675;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU23675
     MX BX BX BX BX B
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                                                                                                                                                                                                                                                                                                                                                                                    Diseases such as alcoholic cirrhosis, biliary cirrhosis, hepatitis, schistosomiasis, cardiac fibrosis, Crohn's disease, diabetic nephropathy and fibroses caused by surgery result from an inappropriate production of collagen fibrils. Collagen III distribent as a preproprotein which is modified by post-translation modification. The mature collagen III fibrils are generated by cleavage of a propeptide from the C-terminus followed by cleavage of a fragment from the N-terminus. This sequence corresponds to the procollagen III C-terminal propeptide (FILICP). As the fibrils are formed the PIIICP propeptide is released into the surrounding tissue fluids. The invention relates to an immunoassay to determine PIIICP concentrations and thus diagnose the above diseases and others which result from inappropriate collagen deposition. Different fibrotic diseases may show different levels of PIIICP in the serum so the
                                                                                                                                                                                                                                                                                                            New immunoassay for procollagen-III-C-terminal propeptide (PIIICP) useful for diagnosing diseases such as alcoholic cirrhosis, hepatitis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunoassay may also be used to determine which disease a particular patient is suffering from. The new immunoassay may also be used to measure the rate of collagen synthesis in patients being treated with glucocorticosteroids. In addition the new antibodies may be used in immunohistochemical staining of cryostat and paraffin sections to assess collagen synthesis in tissue samples from patients suspected of having
                        Alcoholic cirrhosis, biliary cirrhosis, hepatitis, schistosomiasis, cardiac fibrosis, Crohn's disease, diabetic nephropathy, collagen, fibril, procollagen-III-C-terminal propeptide, immunoassay, diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; prey; adipocyte; SID; selected interacting domain; anorectic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 42; DB 2; Length 270; ilarity 100.0%; Pred. No. 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human adipocyte Selected Interacting domain, SID, #444.
                                                                                                                                                                                                                                                 Schroeder W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
Procollagen-III-C-terminal propeptide.
                                                                                                                                                                                                                                                 Neumann R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU70813 standard; protein; 293 AA.
                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1; 28pp; English.
                                                                                                                                                                                                                                                                                                                                      Duchenne's muscular dystrophy.
                                                               glucocorticosteroid; antibody,
                                                                                                                                                                     97EP-00119018.
                                                                                                                                                                                            97EP-00119018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                               Surchardt ER, Kroll W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 IGGEKAGG 19
                                                                                                                                                                                                                                                                        WPI; 1999-256748/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IGGEKAGG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Rest Local Similarity
                                                                                                                                                                                                                      (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                     N-PSDB; AAX57501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 270 AA;
                                                                                                                                                                                             1-OCT-1997;
                                                                                         Homo sapiens
                                                                                                                                                                    31-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-JUN-2003
                                                                                                                 EP913692-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fibrotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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The invention relates to a complex between two interacting proceins in adipocyte cells, given in the specification. The proteins are identified by selecteding a bait protein from a known adipocyte marker and then performing a yeast 2-hybrid selection to isolate prey proteins encoded by conforming a nadipocyte cDNA library. The proceins are designated SID (RTM) (selected interacting demains) proteins. Also included are a complucation of the interacting demains) proteins. Also included are a complucation of the adipocyte cells, a recombinant host cell expressing at least one of the interacting proteins as ID (RTM) polypeptide comprising amy of the 738 amino acid cells, a SID (RTM) polypeptide comprising any of the 738 amino acid sequences given in the specification (including its fragment or variant), a vector comprising the specification (including its fragment or variant), a vector comprising the vector, a protein chip comprising the polypeptides and a recombinant host cell comprising the vector, a protein chip comprising the polypeptides, polynucleotides and compounds are useful for preventing or treating metabolic disorders such as obesity or diabetes. The polynucleotides and subscribed comprising the presenting selected interaction, thus complex, polypeptides, polynucleotides are useful for graventing the therapeutic effect. The present sequence represents a SID (RTM)) for screening drugs that modulate the protein interaction, thus conventing the herapeutic effect. The present sequence represents a SID (RTM) convention of the invariance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New complex between two interacting proteins in adipocyte cells, useful for identifying selected interacting domains that modulate protein interactions, or for preventing or treating metabolic disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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antidiabetic; protein-protein interaction; diabetes; yeast 2-hybrid assay; metabolic disorder; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 258-259; 382pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human enzyme polypeptide #761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU23675 standard; protein; 309 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAR-2002; 2002WO-EP003768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAR-2001; 2001US-0275734P
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Best Local Similarity 100...
Second 8, Conservative
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ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; cytostatic; anti arthritic; nephrotropic; anticoagulant.
                                                                                                                                                                                           2000US-0179065P.
2000US-0186528P.
2000US-0186528P.
2000US-0186174P.
2000US-0198174P.
2000US-0198174P.
2000US-02198175P.
2000US-0215135P.
2000US-0215135P.
2000US-02154319P.
2000US-0217487P.
2000US-0229347P.
2000US-0225268P.
2000US-0225268P.
2000US-0225279P.
2000US-0225279P.
2000US-0225279P.
2000US-0225279P.
2000US-0225344P.
2000US-0229344P.
2000US-0239349P.
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2000US-0232400P.
2000US-0232401P.
2000US-0233063P.
2000US-0233064P.
                                                                                                                                                                    2001WO-US001239
                                                                                                                                                                                            31-JAN-2000) 2-4-FEB-2000; 2-4
                                                                                                                WO200155301-A2
                                                                                                                                                                   17-JAN-2001;
                                                                                       Homo sapiens
                                                                                                                                         02-AUG-2001
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PR 11-SEP 2000 2000US-0234274P.
PR 22-SEP 2000 2000US-023497P.
PR 25-SEP 2000 2000US-023497P.
PR 25-SEP 2000 2000US-023497P.
PR 25-SEP 2000 2000US-023497P.
PR 27-SEP 2000 2000US-023497P.
PR 27-SEP 2000 2000US-023497P.
PR 27-SEP 2000 2000US-023497P.
PR 27-SEP 2000 2000US-023497P.
PR 29-SEP 2000 2000US-023497P.
PR 20-CT-2000 2000US-024447P.
PR 20-CT-2000 2000US-024417P.
PR 20-CT-2000 2000US-024911P.
PR 20-CT-2000 2000

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The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. ALDS) autoimmune disorders (e.g. athritis), neurological disorders (e.g. AlDs) autoimmune disorders (e.g. athritis), cardiovascular disorders (e.g. athreoselenosis), blood-related disorders (e.g. haemophila), reproductive disorders (e.g. infertility) and infectious disorders (e.g. infertility) and infectious disorders (e.g. infertility) and infectious disorders (e.g. infertility) and convention can also be used in gene therapy. AAU22315-AAU23814 represent the novel human enzyme polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but for infertility was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                       Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; SEQ ID NO 1671; 1180pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published pct sequences
                                                                                                                                                                                  Ruben SM;
08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251990P
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                               Barash SC,
                                                                                                                                                                                                                               WPI; 2001-465566/50
                                                                                                                                                                                                                                                            N-PSDB; AAS41545
                                                                                                                                                                               Rosen CA,
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Sequence 309 AA;

Gaps **;** 100.0%; Score 42; DB 4; Length 309; 100.0%; Pred. No. 17; 0; Indels Mismatches ;; 0 Conservative Query Match Best Local Similarity 8; Best Loc Matches

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58 œ 1 IGGEKAGG

51 IGGEKAGG g

ABG60248 standard; protein; 309 AA. 13-AUG-2002 ABG60248 

(first entry)

Human ovarian antigen #10

Human; ovarian antigen; ovary disorder; breast disorder; neoplastic disorder; cancer; infectious disease; inflammatory disease; reproductive system disorder; autoimmune disorder; Alzheimer's disease; blood-related disorder; hyperboliferative disorder; hair loss; urinary system disorder; cardiovascular disorder; arrhythmia; respiratory disorder; nasculoskeletal system disorder; arrhythmia; neural activity disorder; neurological disorder; endocrine disorder; gastrointestinal disorder; large intestine disorder; endocrine di inherited disorder; wound healing; skin aging; food additive; preservative

WO200155329-A2 Homo sapiens

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The invention relates to isolated ovarian related polypeptide (ovarian antigan) comprising a sequence at least 90% identical to a sequence antigan) comprising a sequence at least 90% identical to a sequence selected from a polypeptide fragment, domain, epitope or full length protein of a sequence (S1) appearing as ABG60236 having to related a sequence (S1) appearing as ABG60236 having to relate the cDNA clones encoding the proteins of S1. S1, antibody and the cDNA clones encoding the proteins of S1. S1, reating or ameliorating a medical condition in mammalian subject especially diseases and/or discorders of the ovary and/or breast such as noteinable still diseases (e.g., mastitis, ophoritis), inflammation discorders (such as ovarian Krukenberg tumour and cancer), infectious diseases (e.g., mastitis, ophoritis), inflammatory diseases.

CC discorders (systemic lupus erythematosus, rheumatoid autoimmune disorders (strickle cell anaemia), autoimmune disorders (strickle cell anaemia), arthritis), blood-related disorders (strickle cell anaemia), arthritis), alload-related disorders (strickle cell anaemia), arthritis), anusculoskeletal system disorders (arthrithammatory disorders (Addison's disease) and partineory disorders (Addison's disease) and partineory disorders (Addison's disease), astrointestinal disorders (inflammatory disorders), liver disorders (inflammatory disorders), liver disorders, disorders and wound healing and epithelial cell proliferation. They are also useful to prevent kin aging, for preventing hir loss, to maintain organs conditive or preservative. The present sequence data for comparted and mammalian metabolism, to change a mammal's mental or physical state, and and an epithelial cell proliferation. Note: The sequence data for this patent did not form part of the printed specification, but was conditionally and
                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated human ovarian related polypeptide useful for diagnosis/treatment of disorders of ovary and breast such as neoplastic disorders, infectious diseases, inflammatory diseases, and reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; SEQ ID NO 78; 524pp; English.
                                                                                                                                                                                                                                                                                                                                        Rosen CA, Barash SC, Ruben SM;
                                                                                                   2000US-0179065P.
2000US-0180628P.
2000US-0209467P.
                                                                                                                                                                  2000US-0232398P.
2000US-0249300P.
2000US-0250160P.
                                                                                                                                                                                                                                2000US-0251868P.
2000US-0251990P.
                                                           17-JAN-2001; 2001WO-US001360
                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-476195/51.
                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABK72051
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                                                                                                                                                                                                                                                    08-DEC-2000;
                                                                                                                                           07-JUN-2000;
                                                                                                                                                                                                       01-DEC-2000;
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                                                                                                                                                                                                                                  08-DEC-2000;
                                                                                                      31-JAN-2000;
                   02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorders
                                                                                                                            04-FEB-
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., 0 h 100.0%; Score 42; DB 4; Length 309; Similarity 100.0%; Pred. No. 17; 8; Conservative 0; Mismatches 0; Indels 1 IGGEKAGG 8 Best Local Similarity Query Match Matches

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Gaps

IGGEKAGG 58

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Ovarian related polypeptide; neoplastic disorder; tumour; ovarian cancer; hyperproliferative disorder; adult acute lymphocytic leukaemia; breast cancer; reproductive system disorder; tuberculosis; arthritis; immune system disorder; Chediak-Higashi's synfrome; neonatal neutropenia; autoimmune disorder; Chediak-Higashi's synfrome; neonatal neutropenia; septic shock; multiple sclerosis; central nervous system disorder; neurological disorder; allergy; Parkinson's disease; Alzheimer's disorder; cardiovascular disorder; atherosclerosis; blood related disorder; cardiovascular disorder; innary system disorder; musculoskeletal disorder; osteoporosis; wound healing; endocrine disorder; infectious disease; gastrointestinal disorder; transplantation; food additive; preservative.
                                                                                                                                                             Novel ovarian related polypeptide #10
                                                                  ABG61719 standard; protein; 309 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0179065P.
2000US-0180628P.
2000US-0180638P.
2000US-0189874P.
2000US-0199074P.
2000US-0190076P.
2000US-02515P.
2000US-02515P.
2000US-021515P.
2000US-021515P.
2000US-021515P.
2000US-0217487P.
2000US-0217487P.
2000US-0217487P.
2000US-0217487P.
2000US-0217487P.
2000US-0217487P.
2000US-0217487P.
2000US-0225218P.
2000US-0225218P.
2000US-0225218P.
2000US-0225218P.
2000US-0225218P.
2000US-0225218P.
2000US-0225218P.
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2000US-0225266P.
2000US-0225218P.
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200005-0226219P
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200005-0227182P
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2000US-0229343P.
2000US-0229344P.
2000US-0229345P.
2000US-0229365P.
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                                                                                                                              26-AUG-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JAN-2000, 2
04-FEB-2000, 2
22-MAR-2000, 2
11-MAR-2000, 2
11-MAR-2000, 2
13-MAY-2000, 2
14-MAY-2000, 2
28-UIN-2000, 2
11-UIL-2000, 2
26-UIL-2000, 2
21-AUG-2000, 2
24-AUG-2000, 2
14-AUG-2000, 2
14-AUG
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PR 06-SEP-2000; 2000US-0231431P.
PR 08-SEP-2000; 2000US-0231431P.
PR 08-SEP-2000; 2000US-0231431P.
PR 08-SEP-2000; 2000US-0231431P.
PR 08-SEP-2000; 2000US-0231243P.
PR 12-SEP-2000; 2000US-0231244P.
PR 14-SEP-2000; 2000US-0231308P.
PR 21-SEP-2000; 2000US-0231308P.
PR 20-CCT-2000; 2000US-0231308P.
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The invention relates to a complex between two interacting proceins in adipocyte cells, given in the specification. The proteins are identified by selecting a bait protein from a known adipocyte marker and then competitive a bait protein from a known adipocyte marker and then performing a yeast 2-hybrid selection to isolate prey proteins encoded by compense of an adipocyte cDNA library. The proteins are designated SID (RTM) (selected interacting domains) proteins. Also included are a compluant host cell expressing at least one of the interacting recombinant host cell expressing at least one of the interacting cells, a recombinant host cells expressing any of the 738 amino acid sequences given in the specification (including its fragment or variant), a singly polymucleotide comprising any of the 738 nucleotide sequences given in the specification (including its fragment or variant), a vector comprising the SID (RTM) polymucleotide, a recombinant host cell comprising the Sucception comprising the protein chip comprising the polymeptides and a recombinant host cell comprising and compounds are useful for preventing or treating metabolic disorders such as obesity or diabetes. The complex, polymeledices, polymucleotides and compounds are useful for preventing or treating metabolic disorders such as obesity or diabetes. The polymolectides are useful as probes or primers. The complex is particularly useful for identifying selected interaction, thus certains the therapeutic effect. The present sequence represents a SID (recombined) to the presents as ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New complex between two interacting proteins in adipocyte cells, useful for identifying selected interacting domains that modulate protein interactions, or for preventing or treating metabolic disorders such as obesity or diabetes.
                                                                                     Human; prey, adipocyte, SID; selected interacting domain; anorectic;
antidiabetic; protein-protein interaction; diabetes;
yeast 2-hybrid assay; metabolic disorder; obesity.
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                                                     Human adipocyte Selected Interacting domain, SID, #366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW12843 standard; peptide; 623 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Page 229; 382pp; English.
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                                                                                                                                                                                                                                                                      14-MAR-2002; 2002WO-EP003768
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                 10-JUN-2003 (first entry)
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N-PSDB; ACA57279.
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Best Local Similarity
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                                                                                                                                                                                              WO200286122-A2
                                                                                                                                                              Homo sapiens.
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                                                                                                                                                  2000US-0250160P
2000US-0251391P
2000US-025130BP
2000US-0251988P
2000US-025149P
2000US-0251479P
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2000US-0251869P.
2000US-0251989P.
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2001US-0259678P.
2001US-00764853.
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2001WO-US001339.
2001WO-US001340.
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2001US-00764888
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2001WO-US001334
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(RUBI/) RUBIN S M.
(BARA/) BARASH S C.
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51 IGGEKAGG
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                                                                                                                                                                 01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
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17-NOV-2000;
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RESULT 13 ABU70735 ID ABU7 XX AC ABU7

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This sequence represents a chimeric procollagen molecule of the invention. This sequence has the procollagen C-prepropeptide from the procollagen C-prepropeptide from the propagation attached to the pro-alphal(III) chain sequence. The C-propeptide is implicated in the assembly of the monomer chains into trimerised pro-alpha chains prior to cleavage of the N- and C-propeptides and formation of collagen in fibril-forming procalpha chains. The C-propeptides determine the type-specific assembly of the moieties to which they are attached. The molecule of the invention comprises a first moiety which is an alien collagen clivity attached to a second moiety, which is an alien collagen alpha-chain or a non-collagen material. The novel collagen molecule can be used for treatment or diagnosis in humans cor animals, especially for the treatment of procollagen suicide, as an adhesive or implant, to promote (chronic) wound healing or fibrotic diseases with reduced scarring or for use in photography, brewing, containing substitutions in the recognition site, may have significantly altered properties and characteristics, such as different binding the containing substitutions in the recognition as different binding caltered properties and characteristics, such as different binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel pro:collagen mol. - comprising pro:collagen C-pro:peptide attached to an alien collagen alpha-chain or non-collagen material, useful e.g.
                                                                                  C-propeptide; recognition sequence; procollagen; monomer chain; therapy; trimerised pro-alpha chain; fibril; procollagen suicide; wound healing; fibrotic disease; human; chimeric protein.
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                                                    Pro-alphal(III):(I) CP chimeric protein
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                                                                                                                                                                                                                                                                                                                                                                                          (UYMA-) UNIV VICTORIA MANCHESTER.
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                                                                                                                                                                                                                                                                                                               95GB-00017773.
96GB-00006152.
96GB-00012476.
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               15-DEC-1997 (first entry)
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                                                                                                                                                                      Homo sapiens
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This sequence represents a truncated procollagen pro-alphal(III) chain that can be used in the procollagen molecules of the invention. The C-
trimerised pro-alpha chains prior to cleavage of the monomer chains into trimerised pro-alpha chains prior to cleavage of the N- and C-propeptides and formation of collagen in fibril-forming pro-alpha chains. The C-
propeptides determine the type-specific assembly of the moieties to which they are attached. The molecule of the invention comprises a first moiety having procollagen C-propeptide activity attached to a second moiety, which is an alien collagen alpha-chain or a non-collagen material. The movel collagen molecule can be used for treatment or diagnosis in humans or animals, especially for the treatment of procollagen suicide, as an adhesive or implant, to promote (chronic) wound healing or fibrotic diseases with reduced scarring or for use in photography, brewing, foodstuffs or textiles. The novel collagen molecules, especially when containing substitutions in the recognition site, may have significantly altered properties and characteristics, such as different binding
C-propeptide; recognition sequence; procollagen; monomer chain; therapy; trimerised pro-alpha chain; fibril; procollagen suicide; wound healing; fibrotic disease; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel pro:collagen mol. - comprising pro:collagen C-pro:peptide attach
to an alien collagen alpha-chain or non-collagen material, useful e.g.
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                                                                                                                                                                                                                                                                                                              (UYMA-) UNIV VICTORIA MANCHESTER
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96GB-00006152.
96GB-00012476.
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N-PSDB; AAT59892.
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Best Local Similarity
Matches 8; Conserv
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                                                                                      Homo sapiens
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23-MAR-1996;
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Run on:

September 18, 2004, 04:20:54; Search time 13.1765 Seconds (without alignments)
31.344 Million cell updates/sec

US-10-615-959-40 42 1 IGGEKAGG 8 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

389414 seqs, 51625971 residues Searched:

389414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgn2\_6/ptodata/2/iaa/5A COWB.pep:\*
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
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5: /cgn2\_6/ptodata/2/iaa/pcTUS COMB.pep:\*
6: /cgn2\_6/ptodata/2/iaa/pcTUS COMB.pep:\* Issued Patents AA:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

			Appl	Appl	Appl	Appl	poli	Appli	Appl	26476. A	473052	Appl	Appl	Appl	Appl	4. A		A.	٠.		1. A	App	Appl	Ann	Ann	400	Appl	App1
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		999A-4	999A-4	999A-4	9A-4	4-20	8-3	348-2	-637A-5	-991A-2647		5-21	1-21	3-21	-608-21	-991A-2807	1A-2	1A-2	-991A-2247	1A-2	1A-22	59A-4	3-90	2-90	6	3-90	2-5	2-5
SUMMARIES		6-600-	9-99	56-600-	56-60	08-278-774-20	029-348		9-63	2-95	.20	963-825-	500-811	570-573-2	548-60	252-99	12-99	- 1	2-95	252-99	ė	ij	13-75	586-772	959-51	12-98	'n	5-30
SUMM		. 0	-10-009-	10-00	10-00	08-27	09-0	39-02	US-09-199-	19-25	1052-20	96-86	09-50	09-57	09-54	4	19-252	19-252	÷	4	09-25	08-602-	08-38	98-56	96-80	9-5	-4	08-48
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	Score	42	42	42	42	42	42	42	38	38	36	36	36	36	36	32	34	34	34	33	33	33	32	32	32	32	32	32
	Result No.	-	7	æ	4	Ŋ	9	7	89	o i	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27

Sequence 58, Appl Sequence 58, Appl	Sequence 91, Appl	91,	Sequence 91, Appl	224,	236,		224		1, Ap	Sequence 1, Appli	107			
US-08-476-169-58 US-08-484-083-58	US-08-548-540-91 PCT-US96-09809-91	US-07-963-321-91	US-08-290-641-91 US-08-764-640-236	US-08-973-225-224	US-09-244-298A-236	US-09-516-704-236	US-09-549-090-224	US-09-832-230A-236	US-08-708-893-1	US-09-088-154-1	US-09-489-039A-10730	US-09-252-991A-27476	US-09-252-991A-31304	US-09-252-991A-30746
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5 5 8 7 8	30 31	32	3.4	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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FALCHIA NO. 1904/2401.

FARENLA INFORMATION:

APPLICANT: Eyre, David R.

TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS;

FILE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS;

FILE OF INVENTION NUMBER: US/10/009,999A

CURRENT FILING DATE: 1093-01-22

PRIOR APPLICATION NUMBER: DC1/US99/29357

PRIOR APPLICATION NUMBER: US 09/335,098

PRIOR PLING DATE: 1999-12-10

PRIOR FILING DATE: 1999-06-29

PRIOR PLING DATE: 1999-06-29

PRIOR PLING DATE: 1999-06-29

PRIOR PLING DATE: 1999-06-29

PRIOR PLING DATE: 1999-06-30

PRIOR APPLICATION NUMBER: US 60/142,675

PRIOR APPLICATION NUMBER: US 09/385,740

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: MISC FEATURE OTHER INFORMATION: synthetic peptide corresponding to carboxy-terminal OTHER INFORMATION: telopeptide sequence of human type III collagen
                                                         Sequence 40, Application US/10009999A
Patent No. 6602980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-10-009-999A-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-009-999A-40
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; 0 100.0%; Score 42; DB 4; Length 8; 100.0%; Pred. No. 3e+05; tive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 8; Conservative

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Gaps

à d

US-10-009-999A-41 RESULT 2

; Sequence 41, Application US/10009999A; Patent No. 6602980; Patent INFORMATION: , APPLICANT: Byre, David R. ; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS

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US/08/278,774
                                                                                                                                                                                             Sequence 43, Application US/10009999A Patent No. 6602980 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Palo Alto
California
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                                                        4 IGGEKAGG 11
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Best Local Similarity
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US-08-278-774-20
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GENERAL LICATORANTION

TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS

TITLE REPERENCE: WROS-1-18220

CURRENT APPLICATION NUMBER: US/10/009,999A

CURRENT PILING DATE: 2003-01-22

PRIOR APPLICATION NUMBER: PCT/US99/29357

PRIOR APPLICATION NUMBER: US 09/335,098

PRIOR PILING DATE: 1999-12-10

PRIOR PILING DATE: 1999-06-19

PRIOR FILING DATE: 1999-06-29

PRIOR FILING DATE: 1999-06-29

PRIOR PILING DATE: 1999-06-29

PRIOR PILING DATE: 1999-07-02

PRIOR PILING DATE: 1999-07-02

PRIOR FILING DATE: 1999-07-07

PRIOR SPLING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-08-30

NUMBER OF SEQ ID NOS: 45-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTHER INFORMATION: synthetic peptide corresponding to carboxy-terminal CTHER INFORMATION: telopeptide sequence of human type III collagen US-10-009-999A-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.27;
hea 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 42; DB 4; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 8; Conservative 0; Mismatches 0;
FILE KEKEKENEL WOODS.

CURRENT PELLOKITON NUMBER: US/10/009,999A

CURRENT FILING DATE: 2003-01-22

PRIOR APPLICATION NUMBER: US/10/2095

PRIOR FILING DATE: 1999-10-10

PRIOR FILING DATE: 1999-06-17

PRIOR FILING DATE: 1999-06-29

PRIOR FILING DATE: 1999-06-29

PRIOR FILING DATE: 1999-06-29

PRIOR PILING DATE: 1999-06-29

PRIOR PILING DATE: 1999-06-29

PRIOR APPLICATION NUMBER: US 60/142,675

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-08-30

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PATENT VERSION 3.2

LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-009-999A-42; Sequence 42, Application US/10009999A; Patent No. 6602980
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Best Local Similarity 100.
Matches 8; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MISC FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IGGEKAGG 8
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TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS

FILLE REPERENCE: WROSA-1-18220

CURRENT APPLICATION NUMBER: US/10/009,999A

CURRENT PILING DATE: 1030-10-2

PRIOR FILING DATE: 1999-12-10

PRIOR FILING DATE: 1999-12-10

PRIOR FILING DATE: 1999-06-29

PRIOR FILING DATE: 1999-06-29

PRIOR FILING DATE: 1999-07-02

PRIOR FILING DATE: 1999-07-02

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-08-30

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PALENTIN VERSION 3.2

SOFTWARE: PALENTIN VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , NAME/KEY: MISC FEATURE ; OTHER INFORMATION: synthetic peptide corresponding to carboxy-terminal ; OTHER INFORMATION: telopeptide sequence of human type III collagen US-10-009-999A-43
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Berg, Richard A
APPLICANT: Toman, David P
APPLICANT: Wallace, Donald
TITLE OF INVENTION: MITATED RECOMBINANT COLLAGENS
NUMBER OF SEQUENCES:
ADDRESSEE: COLLAGEN CORPORATION
STREET: 2500 Eaber Place
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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APPLICATT: MALC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                      Gaps
                                                                                                                                                                                      ..
                                            OTHER INFORMATION: Description of Artificial Sequence: SEQUENCE; OTHER INFORMATION: DERIVED FROM cDNA OF PROCOLLAGENS
US-09-029-348-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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90.5%; Score 38; DB 4; Length 674;
Best Local Similarity 75.0%; Pred. No. 67;
Matches 6; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cac., Hui
APPLICANT: Cac., Hui
APPLICANT: Drenkard, Eliana
APPLICANT: Tsongalls, John
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REPRESENCE: 00786/361002
FILE REPRESENCE: 10976/36102
FURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT APPLICATION NUMBER: 1097-11-25
PRIOR FILING DATE: 1998-11-25
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26476, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 51, Application US/09199637A Patent No. 6355411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rahme, Laurence G.
Mahajan-Miklos, Shalina
Tan, Man-Wah
Cao, Hui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick
APPLICANT: Goodman, Howard M.
    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26476
LENGTH: 674
                                                                                                                                                                                                                                                                        368 IGGEKAGG 375
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413 VGGDKAGG 420
                                                                                                             Query Match
Best Local Similarity
8; Conserve
                                                                                                                                                                                                                              1 IGGEKAGG 8
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 42; DB 4; Length 15; 100.0%; Pred. No. 0.36;
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Patent No. 6171827

GENERAL INFORMATION:

APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER

TILLE OF INVENTION: NOVEL PROCOLLAGENS

FILE REFERENCE: 4087857PUS LISTING

CURRENT APPLICATION UNMBER: US/09/029,348

CURRENT FILING DATE: 1998-05-07

NUMBER OF SEQ ID NOS: 2.0

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER
TILLE OF INVENTION: NOVEL PROCCOLLAGENS
FILE REFERENCE: d087857PUS LISTING
CURRENT APPLICATION NUMBER: US/09/029,348
CURRENT FILING DATE: 1998-05-07
NUMBER: OF SEQ ID NOS: 20
SOFTWARE: PALENTIN OVER: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                94-018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 3, Application US/09029348; Patent No. 6171827
                                   ATTORNEY/AGENT INFORMATION:
NAME: RAfayko, Kathi L
REGISTRATION NUMBER: 36,644
REFERENCE/DOCKET NUMBER: 94-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 354-4642
TELERAX: (415) 354-4752
TELERAX: (415) 354-4752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
22-JUL-1994
                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368 IGGEKAGG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IGGEKAGG 8
                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                                                                       linear
FILING DATE: 2;
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                 US-08-278-774-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 3
LENGTH: 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-09-029-348-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-029-348-2
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LENGTH: 626
                                                                                                                                                                                                                                                                                           TYPE:
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FEATURE:

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REGISTRATION NUMBER: 29,714
REFERENCE/DOCKST NUMBER: 43
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
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Similarity 87.5%;
7; Conservative
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TELEX: 236687
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein ORIGINAL SOURCE:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IGGEKAGG
                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                   US-08-963-825-21
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Matches
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; Sequence 21, Application US/08963825
; Patent No. 6110689
; GENERAL INFORMATION:
    APPLICANT: Qvist, Per APPLICANT: Bonde, Martin
    TITLE OF INVENTION: A Method for Assaying Collagen Fragments
    TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of NUMBER OF SEQUENCES: 21
    NUMBER OF SEQUENCES: 22
    NUMBER OF SEQUENCES: 21
    NUMBER OF SEQUENCES: 21
    NUMBER OF SEQUENCES: 21
    STREET: 805 Third Avenue
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                                                                     Gaps
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5473052-20
; Patent No. 5473052
; Patent No. 5473052
; TILL OF INVENTION: ANTIGEN-BINDING FRAGMENTS OF AN ANTIBODY
; TO TYPE-I COLLAGEN AMINO-TERMINAL TELOPEPTIDE
; TO TYPE-I COLLAGEN AMINO-TERMINAL TELOPEPTIDE
; TUTLE OF INVENTES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,705
; FILING DATE: 01-APR-1994
; PRIOR APPLICATION NUMBER: 614,719
; FILING DATE: 01-NOV-1990
; RELING DATE: 01-DEC-1999
; FILING DATE: 01-DEC-1999
; FILING DATE: 01-DEC-1999
; FILING DATE: 06-NOV-1987
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                            DB 4; Length 674;
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87.5%; Pred. No. 2.8;
                                                                     0; Indels
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COMPUTER READABLE FORM:

MEDIUM TYBE: Floppy disk

COMPUTER: The PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/963,825

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                         90.5%; Score 38; DB 75.0%; Pred. No. 67; iive 2; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION UNMERS: US/08/187,319
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: GOGOTIS, Adda C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
        Ouery Match
Best Local Similarity 75...
6; Conservative
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Matches 7; Conservative
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US-08-963-825-21
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REFERENCY. CONTEXT NUMBER: 415c/09101
TELECHRONE. 121:-527-770
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Sequence 21, Application US/09548608
Patent No. 6355442
GENERAL INFORMATION:
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US-09-252-991A-28074
                                       US-09-548-608-21
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APPLICANT: Qvist, Per
APPLICANT: Qvist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
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                                                                                                        Length 1078;
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                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/570,573 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
                                                                                                   Score 36; DB 4; I
Pred. No. 2.3e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: GOGOTIS, Adda C
RECISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                     Sequence 21, Application US/09570573
Patent No. 6342361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (III)
             IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
                                                                                                   Query Match 85.7%;
Best Local Similarity 87.5%;
Matches 7; Conservative
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS;
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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Best Local Similarity 87.5
Matches 7; Conservative
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                                                                                                                                                                                                                             1061 İGAEKAĞĞ 1068
                                                                                                                                                                                     1 IGGEKAGG 8
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                       US-09-500-811-21
                                                                                                                                                                                                                                                                                           RESULT 13
US-09-570-573-21
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Sequence 28074, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPEREBNE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
APPLICANT: Qvist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: A Method and Use of the Method to Diagnose the Presence of
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
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85.7%; Score 36; DB 4; Length 1078;

Best Local Similarity 87.5%; Pred. No. 2.3e+02;

Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/548,608
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4305/08701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/
TELEPHONE: 212-753-6237
TELEPHONE: 212-753-6237
TELERAX: 236697
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Home sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (III)
                                                                                                                                                                                                                                                           805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1061 iGAEKAĞĞ 1068
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TOPOLOGY: linear
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1061 IGAEKAGG 1068

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Search completed: September 18, 2004, 04:32:21 Job time: 14.1765 secs

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Sequence 41, Appl
Sequence 42, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 226, Appl
Sequence 72, Appl
Sequence 72, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 11, Appl
                                                                                                                                September 18, 2004, 04:29:56; Search time 37.9608 Seconds (without alignments) 67.677 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-615-959-41

US-10-615-959-43

US-10-615-959-43

US-10-366-125-11

US-10-366-125-19

US-09-908-711-78

US-09-908-711-78

US-10-257-021-72
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US-10-734-564-103
US-10-402-089-12
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Maximum Match 100%
Listing first 45 summaries
                                                                                       OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                                                                                                                                                                             Sequence:
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                                                                                                                                     Run on:
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Seguence 12, Appl		ເກ	7	equence 1	equence 1	2	equence 1	7849,	Sequence 21, Appl	27910	Sequence 189501,	Sequence 61090, A	Sequence 157383,	equenc	Sequence 6, Appli	Sequence 18766, A	Sequence 19844, A	Sequence 21046, A	Sequence 2735, Ap	18807		4	9	4	9	guence 380	Sequence 185108	e 1963	10781
10-402-072	-10-437-96	-09-975-719-	-437-963	10-437-963	-10-437-963	-10-424-599-	10-424-599-	-10-156-761-784	10-058-1	-10-424-599-2791	-10-437-963-1895	10-425-114-6109	-10-437-963-15	10-214-473-6	-10 - 272 - 490	-10-369-493-1	10-369-493-1984	10-369-493-210	US-10-369-493-2735	-437-963-18807	US-10-282-122A-47568	-10-402-		-402-072A	US-10-402-072A-6	09-864-761-3	-10-424-599-18510	10-437-963-196	-10-437-963-10781
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16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43		

## ALIGNMENTS

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RESULT INCRANCE 15-59-40

Sequence 40, Application US/10615959

Publication No. 1202040048321A1

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
PRICE REFERENCE: WROS-1-1820

CURRENT ELING DATE: 2003-07-08

PRIOR PRILING DATE: 2003-07-08

PRIOR APPLICATION NUMBER: US/10/09,99A

PRIOR FILING DATE: 1999-10-12

PRIOR PELING DATE: 1999-10-12

PRIOR PELING DATE: 1999-06-19

PRIOR PELING DATE: 1999-06-19

PRIOR PELING DATE: 1999-06-19

PRIOR PELING DATE: 1999-06-19

PRIOR PELING DATE: 1999-06-29

PRIOR PELING DATE: 1999-06-29

PRIOR PELING DATE: 1999-07-07

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PRIOR PELING DATE: 1999-07-07

PRIOR PELING DATE:
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100.0%; Score 42; DB 12; Length 8; 100.0%; Pred. No. 1.2e+06;

Query Match Best Local Similarity ö

Gaps

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US-10-b15-959-43
; Sequence 43, Application US/10615959
; Publication No. US20040048321A1
; GENERAL INFORMATION:
APPLICANT: BYTE, David R.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS
; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS
; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS
; CURRENT APPLICATION NUMBER: US/10/009,999A
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: PCT/US99/29357
; PRIOR APPLICATION NUMBER: PCT/US99/29357
; PRIOR APPLICATION NUMBER: US 60/141,574
; PRIOR FILING DATE: 1999-06-17
; PRIOR FILING DATE: 1999-06-17
; PRIOR FILING DATE: 1999-07-02
; PRIOR PLICATION NUMBER: US 60/142,675
; PRIOR APPLICATION NUMBER: US 60/142,675
; PRIOR PLILING DATE: 1999-07-07
; PRIOR PLILING DATE: 1999-07-07
; PRIOR PLILING DATE: 1999-07-07
; PRIOR PLILING DATE: 1999-07-07
; PRIOR FILING DATE: 1999-07-07
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                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: synthetic peptide corresponding to carboxy-terminal OTHER INFORMATION: telopeptide sequence of human type III collagen
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100.0%; Score 42; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 0; Indels
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 09/385,740
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
SEQ ID NO 42
LYPE: PRT
TYPE: PRT
TYPE: PRT
ORGANISM: Homo sapiens
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 43
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Best Local Similarity 100.
Matches 8; Conservative
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US-10-366-125-11
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APPLICANT: BYTE, David R.
TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS
FILE REFERENCE: WROS-1-1820
CURRENT APPLICATION NUMBER: US/10/615,959
CURRENT PILING DATE: 2003-07-08
PRIOR PELICATION NUMBER: US/10/009,999A
PRIOR PELICATION NUMBER: PCT/US99/29357
PRIOR PELICATION NUMBER: US/00/335,098
PRIOR PILING DATE: 1999-06-17
PRIOR PILING DATE: 1999-06-17
PRIOR PILING DATE: 1999-06-17
PRIOR PELICATION NUMBER: US 60/141,574
PRIOR APPLICATION NUMBER: US 60/142,274
PRIOR PILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-07
PRIOR FILING DATE: 1999-06-07
PRIOR FILING DATE: 1999-06-07
PRIOR FILING DATE: 1999-06-07
PRIOR FILING DATE: 1999-08-30
PRIOR FILING DATE: 1999-08-30
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PRIOR PRIOR PELING DATE: 1999-08-30
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TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS
FILE REPERENCE: WROS4-1-18220
CURRENT APPLICATION NUMBER: US/10/615,959
CURRENT FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: US/10/009,999A
PRIOR PILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: US/10/009,9357
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 09/335,098
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: US 60/141,574
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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; Sequence 42. Application US/10615959
; Publication No. US20040048321A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                    Sequence 41, Application US/10615959; Publication No. US20040048321A1; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 8; Conservative
                          8; Conservative
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ORGANISM: Homo sapiens
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US-10-615-959-41
                             Matches
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TITLE OF INVENTION: MEASUREMENT OF BIOSYNTHESIS AND BREAKDOWN RATES OF

TITLE OF INVENTION: BIOLOGICAL MOLECULES THAT ARE INACCESSIBLE OR NOT

TITLE OF INVENTION: BASILY ACCESSIBLE TO DIRECT SAMPLING, NON-INVASIVELY,

TITLE OF INVENTION: CATABOLITIC PRODUCTS

TITLE OF INVENTION: CATABOLITIC PRODUCTS

FILE REFERENCE: 41627203500

CURRENT APPLICATION NUMBER: US/10/366,125

CURRENT APPLICATION NUMBER: US 60/356,008

PRIOR PALING DATE: 2002-02-12

PRIOR PALING DATE: 2002-02-12

NUMBER OF SEQ ID NOS: 28

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 262
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         APPLICANT: Hellerstein, Marc
TITLE OF INVENTION: MEASUREMENT OF BIOSYNTHESIS AND BREAKDOWN RATES OF
TITLE OF INVENTION: BIOLOGICAL MOLECULES THAT ARE INACCESSIBLE OF NOT
TITLE OF INVENTION: BASILY ACCESSIBLE TO DIRECT SAMPLING, NON-INVASIVELY,
TITLE OF INVENTION: BY LABEL INCORPORATION INTO METABOLIC DERIVATIVES AND
TITLE OF INVENTION: CATABOLITIC PRODUCTS
FILE REFERENCE: 416272003500
CURRENT APPLICATION NUMBER: US/10/366,125
CURRENT PAPLICATION NUMBER: US/00/366,126
PRIOR PRIOR PALLING DATE: 2002-02-12
PRIOR FILING DATE: 2002-02-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 42; DB 15; Length 25; 100.0%; Pred. No. 3.6;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFRENCE: PAL28
CURRENT APPLICATION NUMBER: US/09/908,711
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US01/01360
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 25
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Publication No. US20030228259A1
GENERAL INFORMATION:
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Patent No. US20020045230A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 8; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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Matches 8; Conserv
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PRIOR APPLICATION NUMBER: 09/764,867
PRIOR FILING DATE: 2001.01.71
PRIOR PELICATION NUMBER: 09/764,892
PRIOR FILING DATE: 2001.01.71
PRIOR PELICATION NUMBER: 09/764,892
PRIOR PELICATION NUMBER: 09/764,892
PRIOR PELICATION NUMBER: 09/764,989
PRIOR PELING DATE: 2001.01.77
PRIOR APPLICATION NUMBER: 09/764,905
PRIOR PELING DATE: 2001.01.77
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PRIOR PELING DATE: 2001.01.77
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PRIOR APPLICATION NUMBER: 097764, 866
PRIOR PELING DATE: 2001.01.77
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PRIOR APPLICATION NUMBER: 097764, 866
PRIOR PELING DATE: 2001.01.77
PRIOR APPLICATION NUMBER: 0997764, 866
PRIOR PELING DATE: 2000.01.77
PRIOR APPLICATION NUMBER: 099776
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Myer, Vic
Wang, Youzhen
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APPLICANT: Glatt, Karen
APPLICANT: Zhao, Xumei
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US-10-177-293-68
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US-10-177-293-68
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                                                                                                                            LOCATION: (2)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                ; LOCATION: (4)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-908-711-78
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                                                                                                                                                                                                                                                                         100.0%; Score 42; DB 9; Length 309; 100.0%; Pred. No. 40; cive 0; Mismatches 0; Indels
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Sequence 226, Application US/09918715

Sequence 226, Application US/09918715

SEQUENCE ON O. US20030017157A1

SEPLICANT: Brad St. Croix

APPLICANT: Bert Vogelstein

APPLICANT: Renneth Kinzler

TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS

FILE REPRENCE: 1107.00134

CURRENT APPLICATION NUMBER: 05/22,599

PRIOR APPLICATION NUMBER: 60/224,360

PRIOR PILING DATE: 2000-08-01

PRIOR PILING DATE: 2000-08-11

PRIOR FILING DATE: 2000-08-11

PRIOR FILING DATE: 2000-04-11

PRIOR FILING DATE: 2000-04-11

PRIOR FILING DATE: 2000-04-11

SEQ ID NOS: 358

SOFTWARE: FastSEQ for Windows Version 3.0
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Publication No. US20030211498A1

GENERAL INFORMATION:

APPLICANT: Blerman-Baust, Cheryl A.

APPLICANT: Blerman-Baust, Cheryl A.

APPLICANT: Blerman-Baust, Cheryl A.

APPLICANT: Blerman-Baust, Cheryl A.

FILE REFERENCE: 14014, O3169U2

TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER

FILE REFERENCE: 14014, 03369U2

CURRENT APPLICATION NUMBER: US/10/257,021

CURRENT FILING DATE: 2001-04-03

PRIOR FILING DATE: 2001-04-03

PRIOR FILING DATE: 2001-04-03
                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 8; Conservative
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SEQ ID NO 78
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 8; Conservat
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                                                                                                              NAME/KEY: SITE
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1208 İĞĞEKAĞĞ 1215
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US-10-734-564-103
                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo Sapien
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US-10-402-089-12
US-10-358-024-3
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                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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                                                      Sequence 33, Application US/10301822

Publication No. US20030148410A1

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: Millentete, Tracy L.

APPLICANT: Monaban; John E.

APPLICANT: Schlegel, Robert

APPLICANT: Monaban; John E.

APPLICANT: Monaban; John E.

APPLICANT: Thibodeau, Stephen N.

APPLICANT: Thibodeau, Stephen N.

APPLICANT: Thibodeau, Stephen N.

APPLICANT: Thibodeau, Stephen N.

APPLICANT: Thibodeau, Stephen N.

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND

TITLE OF INVENTION: THERAPY OF COLON CANCER

FILE REFERENCE: MPNO1-023P2RNM

CURRENT APPLICATION WHOBER: US 60/339,971

PRIOR APPLICATION WHOBER: US 60/331,978

PRIOR APPLICATION NUMBER: US 60/331,978

PRIOR APPLICATION NUMBER: US 60/331,978

PRIOR APPLICATION NUMBER: US 60/331,988

PRIOR PILING DATE: 2002-05-03

NUMBER OF SEQ ID NOS: 228

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 33

LENGTH: 1466.
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TILE OF INVENTION: Method and Compositions Involving
TITLE OF INVENTION: T-Lymphocyte Reactivity with Collagen in Aortic Tissue of
TITLE OF INVENTION: T-Lymphocyte Reactivity with Collagen in Aortic Tissue of
TITLE OF INVENTION: Abdominal Aortic Aneurysm Patients
CURRENT APPLICATION NUMBER: 02(10/357,851
CURRENT APPLICATION NUMBER: 2003-02-04
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0.
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Best Local Similarity 100.
Matches 8; Conservative
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CRGANISM: Homo Sapiens
US-10-357-851-3
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US-10-301-822-33
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                                              -10-301-822-33
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US-10-357-851-3
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Sequence 3, Application US/10358024
Publication No. US20040151732A1
GENERAL INFORMATION:
APPLICANT: Jicha, Douglas L.
APPLICANT: Felsue, Stephen
TITLE OF INVENTION: T-Lymphocytes Reactivity with Collagen
FILE REFERENCE: 13436US
CURRENT APPLICATION NUMBER: US/10/358,024
CURRENT FILING DATE: 2003-02-04
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Publication No. US2004000563A1
GENERAL INFORMATION:
APPLICANT: Bell, Marcum P.
APPLICANT: Bell, Marcum P.
APPLICANT: Bell, Marcum P.
APPLICANT: Seeley, Todd W.
TITLE OF INVENTION: PORCINE COLLAGENS AND GELATINS
FILE REFERENT PORTO: FP0402.3 CON
CURRENT FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: US 09/709,700
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-734-564-103

Sequence 103, Application US/10734564

Publication No. US20640157278A1

GENERAL INFORMATION:

APPLICANT: Christopher C Burgess et al

TITLE OF INVENTION: Detection Methods Using TIMP1

FILE REFERENCE: 1657/2012

CURRENT APPLICATION NUMBER: US/10/734,564

CURRENT FILING DATE: 2003-12-12

NUMBER OF SEQ ID NOS: 138

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 103

LENGTH: 1466
                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 42; DB 16; 100.0%; Pred. No. 1.8e+02;
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100.0%; Pred. No. 1.8e+02;
trive 0; Mismatches 0;
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Best Local Similarity 100...
8; Conservative
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Best Local Similarity 100.
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SOFTWARE: Patentin version 3.2

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; SEQ ID NO 12
; INNCH: 1466
; ITYPE: PRT
; ORGANISM: Sus scrofa
US-10-402-089-12
Query Match
Best Local Similarity 87.5%; Pred. No. 2.6e+02;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps
Qy 1 IGGEKAGG 8
:||||||||
Db 1208 VGGEKAGG 1215
Search completed: September 18, 2004, 04:56:12
JOb time : 38.9608 secs
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0;

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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sw model protein search, using OM protein

Run on:

September 18, 2004, 04:02:05; Search time 9.72549 Seconds (without alignments) 79.125 Million cell updates/sec

US-10-615-959-40 42 1 IGGEKAGG 8 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* PIR 78:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	alpha	collagen alpha 1(I	alpha	ical pr	_		hypothetical prote	heat shock protein	formylmethanofuran	formylmethanofuran	phosphoglucomutase	hypothetical prote	⊣	- 14	cis-1,2-dihydro-1,	probable phosphogl	ribonucleoside-dip	ABC excision nucle	hypothetical prote	probable membrane	carboxylesterase (	probable linase (E	probable lipase/es	riboflavin biosynt	SETTIMO	anthranilate phosp		۲,	arylesterase [impo
DB ID					2 \$56535									2 B36724	•		1 WMBEB1	2 T36039	2 T47394	2 AD0306		2 I39567		2 E96972				ഗ	AE
Query Match Length D	1466	636	1464	476	404	404	404	161	270	270	475	490	165	240	266	470	1137	113	163	295	311	364	376	383	478	773	126	155	209
Query Match	100.0	90.5	90.5	88.1	85.7	85.7	85.7						81.0	81.0	81.0	81.0	81.0	78.6	78.6	•	78.6	78.6	78.6					76.2	
Score	42	38	38	37	36	36	36	35	32	35	32	35	34	34	34	34	34	33	33	33	33	33	33	33	33	33	32	32	32
Result No.	н	7	m	4	2	9	7	æ		10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

arylesterase (AF04	hypothetical prote	phenazine biosynth	TAX responsive ele	ribosomal protein	TAXREB107 - human	GRESAG protein 9u	ribosomal protein	conserved hypothet	hypothetical prote	hypothetical prote	carboxylesterase B	conserved hypothet	probable S2P metal	conserved hypothet	serine/threonine-s
C98302	T49037	C87648	S55922	833714	I51803	B39581	T50782	F81016	T20497	C96533	F84000	D81961	G72777	C82159	T49152
7	~	7	~	7	N	N	7	7	7	7	7	~	~	~	7
209	233	275	287	288	288	296	297	302	316	319	321	328	383	384	386
76.2	76.2	76.2	76.2	76.2	76.2	76.2	76.2	76.2	76.2	76.2	76.2	76.2	76.2	76.2	76.2
	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32
32															

# ALIGNMENTS

Affections of the control of the control of the human type-III procollagen gene A; Reference number: PE0011; MUID:89378752; PMID:2777083

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Ajaccession: PE001 Ajmolecule type: DNA Ajrestiucs: 1-176 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrestiucs: 1-1726 <br/>Ajrest

A; Accession: S01726

A; Molecule type: mRNA A; Residues: 1-170 < TOMA A; Cross-references: EMBL:X07240; NID:g30060; PIDN:CAA30229.1; PID:g30061 A; Cross-references: EMBL:X07240; NID:g30060; PIDN:CAA30229.1; PID:g30061 A; Vaneczko, R.A.; Ramirez, F. Nucleic Acids Res. 17, 6742, 1989 A; Title: Nucleotide and amino acid sequences of the entire human alpha-1 (III) collagen. A; Reference number: \$04887; MUID:89386015; PMID:2780304

A, Accession: S04887

A,Molecule type: mRNA A,Rosidues: 149-163, 'G',164-240, 'D',242-471, 'D',473-487, 'L',489,'S',491-613,'Y',615-634,' A,Cross-references: EMBL:X15332; NID:g29545; PIDN:CAA33387.1; PID:g930045 A,Note: the authors' translation of residues 905-932 is inconsistent with the nucleotide R,Seyer, J.M.; Kang, A.H.

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A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 950-1018,'Y',1020-1183,'S',1185-1466 <MAN>
A;Cross-references: EMBL:X06700; NID:g30053; PIDN:CAA29886.1; PID:g30054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Gene: GDB:COL3A1
A,Cross-references: GDB:118729; OMIM:120180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                         R,Seyer, J.M.; Kang, A.H.
Biochemistry 20, 2621-2627, 1981
A,Title: Covalent structure of c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Molecule type: mRNA
A; Residues: 1165-1196 < EMA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Accession: I79359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: A92516
                                                                                                                                                                                                                                                                                                        A; Accession: A90446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
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                                                                                          Biochemistry 16, 1158-1164, 1977
A;Title: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptide
A;Reference number: A90399; MUID:77134724; PMID:557335
                                                                                                                                                                                                                                                                                                                                                                            A,Reference number: A94562
A,Accession: A94562
A,Accession: A94562
A,Accession: A94562
A,Molecule type: protein
A,Experimental source: liver
A,Note: auchor submitted corrections to A90399
R,Milwaicz, D.M.; Witz, A.M.; Smith, A.C.; Manchester, D.K.; Waldstein, G.; Byers, P.H. Am. Genet. S3, 62-70, 1993
A,Title: Parental somatic and germ-line mosaicism for a multiexon deletion with unusual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: IS1868; MUID:93304430; PMID:8317500
A;Accession: IS1868
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                 submitted to the Atlas, December 1977
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A; Molecule type: protein
A;Residues: 965-979,'A',981-984,'PS',987,'QN',990-1096,'P',1098-1152,'AT',1155,'S',1157-1
A;Experimental source: liver
R;Loidl, H.R.; Brinker, J.M.; May, M.; Pihlajaniemi, T.; Morrow, S.; Rosenbloom, J.; Myel Nucleic Acids Res. 12, 9383-9394, 1984
A;Title: Molecular cloning and carboxyl-propeptide analysis of human type III procollages
A;Reference number: A93551; MUID:85087944; PMID:6096827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Wolecule type: mRNA
A; Residues: 1065-1155, 'P',1157-1466 <LOI>
A; Residues: 1065-1155, 'P', 1157-1466 <LOI>
A; Cross-references: EMBL.X01655; EMBL:X01742; NID:929584; PIDN:CAA25821.1
R; Miskulin, M.; Dalgleish, R.; Kluve-Beckerman, B.; Rennard, S.I.; Tolstoshev, P.; Brantl
B; Miskulin, M.; Dalgleish, R.; Kluve-Beckerman, B.; Rennard, S.I.; Tolstoshev, P.; Brantl
R; Miskulin, M.; Dalgleish, R.; Kluve-Beckerman, B.; Rennard, S.I.; Tolstoshev, P.; Brantl
R; Miskulin, M.; Jalgleish, R.; Millo: Beckerman, B.; Rennard, S.I.; Tolstoshev, P.; Brantl
A; Reference number: 152393; MUID: 86187804; PMID: 3754462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: translated from GB/EWBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: l16f-1200 <MIS>
A;Cross-references: GB:M13146; NID:g180415; PIDN:AAA52003.1; PID:g180416
A;Cross-references: GB:M13146; NID:g180415; PIDN:AAA52003.1; PID:g180416
A;Cross-references: GB:M13146; NID:g180415; PIDN:AAS52003.1; PID:g180416
A;Cross-references: GB:M13146; NID:g180415; PIDN:APSECO: Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
A;Title: Human alpha 1(III) and alpha 2(V) procollagen genes are located on the long arm A;Reference number: I59025; MUID:85216505; PMID:3858826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: the authors translated the codon TTC for residue 1057 as Tyr; the codons given for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit (( 3-hydroxylated and some are subsequently O
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A,Introns: 27/1: 94/3: 111/3: 149/3: 176/3: 554/3: 587/3: 1175/3: 1275/1: 1337/3: 1418/3
A,Introns: 27/1: 94/3: 111/3: 149/3: 176/3: 554/3: 587/3: 1175/3: 1275/1: 1337/3: 1418/3
A,Note: the list of introns is incomplete; defects in this gene can result in Ehlers-Danla, C,Complex: type III collagen is a homotrimer of monomers initially linked by disulfide bc or of their length, is formed with desmosine cross-links made from lysine and allysine re
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A;Reference number: A90446; MUID:81208139; PMID:7016180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1176-1240,'V',1242-1356,'P',1358-1466 <CHU>
A;Cross-references: GB:M10615; GB:M10793; GB:M10794; GB:M10795; GB:M10796; GB:M10797; GB
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R;Chu, M.L.; Weil, D.; de Wet, W.; Bernard, M.; Sippola, M.; Ramirez, F.
d, Biol. Chem. 260, 4357-4363, 1985
A;Title: Isolation of cDNA and genomic clones encoding human pro-alphal(III)
A;Reference number: A92516; MUID:85157600; PMID:2579949
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F;1091-1093/Region: cell attachment (R-G-D) motif
F;1197-1221/Region: carboxyl-terminal nonhelical telopeptide
F;1222-1466/Domain: carboxyl-terminal propeptide #status predicted <CPR>F;1238-1466/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
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C;Accession: Ag1031
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, L. T. Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Authors: Parry C.
A;Aitle: Complete genome sequence of a multiple drug resistant Salmonella enterica serove A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ## Sintrons: 29/1; 95/3; 112/3; 150/3; 175/3; 193/3; 211/3; 229/3; 247/3; 265/3; 281/3; 298/3; 673/3; 706/3; 706/3; 706/3; 718/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3; 818/3
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A;Residues: 1-866,'G',868-1464 <TOA>
A;Cross-references: EMBL:X22046, NID:g575321; PIDN:CAA36279.1; PID:g575322
R;Mctsaeranta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E.
Biochim. Biophys. Acta 1089, 241-243, 1991
Biochim. Biophys. Acta 1089, 241-243, 1991
A;Tutle: Specific hybridization probes for mouse type I, II, III and IX collagen mRNAs.
A;Reference number: S16176; MUID:91274355; PMID:2054384
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A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                           submitted to the EMBL Data Library, November 1994 A;Reference number: $62120 A;Accession: $62120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 63;
2; Mismatches
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Pred. No. 34;
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75.0%;
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                                                                                              A;Residues: 1-1464 <TOM>
A;Cross-references: EMBL:X52046
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A;Molecule type: DNA
A;Residues: 1442-1464 <MET>
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1206 VGGEKSGG 1213
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                                                                    A; Molecule type: DNA
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F;24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted F;153-154/Cleavage site: Pro-Gln (procollagen N-endopeptidase) #status predicted F;154/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicte F;161,1212/Modified site: allysine (Lys) #status predicted F;263,284,860,977,1106/Modified site: 5-hydroxylysine (Lys) #status experimental F;263,284,860,977,1106/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental F;584,1094/Modified site: 6-hydroxylysine (Lys) (partial) #status experimental F;948-949/Cleavage site: Gly-11e (collagenase) #status experimental F;948-949/Cleavage site: Gly-11e (collagenase) #status predicted
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C;Species: Mis musculus (house mouse)
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
C;Constant, D:D: de Crombrugghe, B.
Gene 147, 161-168, 1994
A;Title: The mouse type-III procollagen-encoding gene: genomic cloning and complete DNA A;Reference number: S59856; MUID:95011609; PMID:7926795
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C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
C;Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix
F;408-636/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
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C;Species: Rattus norregicus (Norway rat)
C;Species: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 13-Aug-1999
C;Accession: S41067; A29905; S31924
R;Glumoff, V.; Maekelae, J.K.; Vuorio, E.
Biochim. Biophys. Acta 1217, 41-48, 1994
A;Title: Cloning of cDNA for rat pro alpha-1(III) collagen mRNA. Different expression A;Reference number: S41067; MUID:94114571; PMID:8286415
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R;Frankel, F.R.; Hsu, C.Y.J.; Myers, J.C.; Lin, E.; Lyttle, C.R.; Komm, B.; Mohn, K.
DNA 7, 347-354; 1988
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A;Accession: A29905
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VGGEKSGG 385
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A;Residues: 308-482 <FRA>
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Matches 8; Conserv
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A;Molecule type: mRNA
A;Residues: 1-636 <GLU>
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A,Molecule type: mRNA
A,Residues: 2-636 <GL2>
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A; Accession: S31924

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RESULT 3 **S**59856

Query Match Matches

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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, iller, L.; Grotbeck, B.J.; Davië, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H86128
A;Accession: H86128
A;Accession: Liminary
A;Molecule type: DNA
                                                                                                                                                                                                      A,Residues: 1.404 <STO>
A;Cross-references: GB:AE005174; NID:g12519317; PIDN:AAG59492.1; GSPDB:GN00145; UWGP:Z590
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: yihT
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C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Sep-1999
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Discrete Concerte-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; F. S. Santh, D.R.; Doucette-Stamm, L.A.; Mang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N., Qiu, D.; Spadafora, R.; Vicaire, R.; Mang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N., ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. A.; Lacteriol. 179, 7135-7155, 1997

A.Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A; Reference number: A69000; MUID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-270 <MTH>
A;Cross-references: GB:AE000916; GB:AE000666; NID:g2622674; PIDN:AAB86032.1; PID:g262268
A;Experimental source: strain Delta H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Zea mayB (maize)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C;Accession: S1499B
C;Accession: S1499B
B;Gpping, I.S.; Frappier, J.R.H.; Walden, D.B.; Atkinson, B.G.
Plant Mol. Biol. 16, 699-711, 1991
A;Tille: Sequence, identification and characterization of cDNAs encoding two
A;Reference number: S14997; MUID:91329703; PMID:1714322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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C;Keywords: iron-sulfur protein; metalloprotein; oxidoreductase; tungsten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X54076; NID:g22338; PIDN:CAA38013.1; PID:g22339
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Pred. No. 29;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB 2
Pred. No. 44;
0; Mismatches
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C;Keywords: heat shock; stress-induced protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - maize
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Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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A; Residues: 1-161 <GOP>
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H86128
hypothetical protein yjhT [imported] - Escherichia coli (strain O157:H7, substrain EDL93
c) Specials: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: H86128
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-404 < BUR.
A; Residues: 1-404 < BUR.
A; Cross-references: EMBL:U14003; NID:g1263172; PIDN:AAA97206.1; PID:g537151
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc.
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
                    intergenic region) - Escherichia coli (strain K-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gend
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Ω.
                            hypothetical 43.7K protein (fecI-fimB intergenic region) - Bscherichia coli (strain K-12 NgAlternate names: hypothetical protein f404
C;Species: Secherichia coli coli f404
C;Species: Secherichia coli coli a coli 3.Nov-1995 #text_change 01-Mar-2002
C;Accession: S56535; M5524
R;Burland, V.; Plunkett III G; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.
A;Reference number: S56314; MuID:95334362; PMID:7610040
A;Accession: S56555
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Accession: H65244
A) Status: preliminary; nucleic acid sequence not shown; translation not shown
A, Molecule type: DNA
A, Residues: 1-404 < BLAT>
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Pred. No. 44;
0; Mismatches 1; Indels
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Pred. No. 44;
0; Mismatches
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Best Local Similarity 8/...
7; Conservative
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377 IGGETAGG 384
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IGGETAGG 384

377

1 IGGEKAGG 8

8 g

A; Gene: yjhT

1 IGGEKAGG 8

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Similarity 7; Conserv

Query Match Best Local S Matches 7

A, Gene: ECs5269

1-404 <HAY>

A, Status: preliminary A, Molecule type: DNA A, Residues: 1-404 <HAN

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Gispedies: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S7539
C;Azcession: S7539
C;Azcession: S7539
C;Azcession: S7539
C;Azcession: S7539
C;Azcession: S7539
C;Azcession: S7; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-490 -KAN>
A;Cross-references: EMBL:D90911; GB:AB001339; NID:g1653083; PIDN:BAA18100.1; PID:g165318;
A;NOTe: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: phosphomannomutase
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A,Residues: 1-165 <WOO>
A,Cross-references: EMBL:AL031824; PIDN:CAA21221.1; GSPDB:GN00068; SPDB:SPCC31H12.04c
A,Experimental source: strain 972h-; cosmid c31H12
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A;Cross-references: EMBL:AL031535; PIDN:CAA20752.1; GSPDB:GN00068; SPDB:SPCC16C4.13c
A;Experimental source: strain 972h-; cosmid c16C4
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
Submitted to the EMBL Data Library, September 1998
A;Reference number: Z21985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T41103
60s ribosomal protein 112 - fission yeast (Schizosaccharomyces pombe)
61s ribosomal protein 112 - fission yeast (Schizosaccharomyces pombe
6. Species: Schizosaccharomyces pombe
6. Accession: T41103; T41292
7. Schoression: T41103; T41292
7. Structure 11292
7. Structure 11292
7. Structure 11292
8. School 1220364
8. Reference number: Z21964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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hypothetical protein slr1334 - Synechocystis sp. (strain PCC 6803)
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                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: $74322; MUID:97061201; PMID:8905231
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81;
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A;Molecule type: DNA
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A;Molecule type: DNA
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Pred. No. 45;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.0%; Score 34; 75.0%; Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: SPCC16C4.13c; SPCC31H12.04c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.v.,
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VGGEVAGG 25
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Best Local Similarity
Matches 6; Conserv
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A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Methanobacterium thermoautotrophicum (C;Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 20-Jun-2000 (C;Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 20-Jun-2000 (C;Accession: 863546; 857457 (C;Accession: 863546; 8575457 (C;Accession: 863546; 8575457 (C;Accession: 863546; 8575457 (C;Accession: 863546; 8575457 (C;Accession: 863546; 8575457 (C;Accession: 863546; 8575452 (C;Accession: 863546; 8575452 (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546) (C;Accession: 863546)
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C;Keywords: heterotetramer; iron-sulfur protein; metalloprotein; oxidoreductase; tungste
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                      - Methanobacterium the
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A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X87970; NID:g1890205; PIDN:CAA61214.1; PID:g1890211
A;Experimental source: strain Marburg, DSM 2133
                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                      formylmethanofuran dehydrogenase (EC 1.2.99.5) (tungsten) chain C
                               Length 270,
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83.3%; Score 35; DB 2; Length 270;
Best Local Similarity 75.0%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 1; Indels
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83.3%; Score 35; DB 2; Length 475;
Best Local Similarity 75.0%; Pred. No. 79;
Matches 6; Conservative 2; Mismatches 0; Indels
                                                                                                      1; Indels
                               5;
                               DB 47;
                                                                                                      1; Mismatches
                               Score 35;
Pred. No.
                           83.3%;
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A,Gene: all3964
C,Superfamily: phosphomannomutase
                                                                                                  6; Conservative
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200 VGGEMAGG 207
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200 VGGEMAGG 207
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                       Query Match
Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-270 <HOC>
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A; Residues: 1-475 < KUR>
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A; Status: preliminary
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S75539
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R;Behrmann, I.; Hillemann, D.; Puehler, A.; Strauch, E.; Wohlleben, W.
J. Bacteriol. 172, 5326-5334, 1990
A;Title: Overexpression of a Streptomyces viridochromogenes gene (glnII) encoding a glut yl-alanine.
A;Telence number: A36724; MUID: 90368592; PMID: 1975583
A;Accession: B36724
A;Status: preliminary
A;Reference number: A36724; MUID: 90368592; PMID: 1975583
A;Reference: Exeliminary
A;Residues: 1-240 cBEH>
A;Residues: 1-240 cBEH>
A;Cross-references: EMBL: X52842; NID: g47983; PIDN: CAA37027.1; PID: g47985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cjaccesion: T31264
R;Romine, M. P.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; G submitted to the EMBL Data Library, July 1998
A;Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromatian Reference number: Z20992
A;Reference number: Z20992
A;Reference number: Z20992
A;Reference number: J2564
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: DNA
A;Residues: 1-266 cROM>
A;Residues: 1-266 cROM>
A;Cross-references: EMBL:AF079317; NID:g3378261; PID:g3378405; PIDN:AAD03988.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cis.1,2-dihydro-1,2-dihydroxynaphthalene dehydrogenase homolog - Sphingomonas aromaticiv
C,Species: Sphingomonas aromaticivorans
C,Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
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A;Genome: plasmid pNL1
A;Note: bphB
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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81.0%; Score 34; DB 2; Length 240;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 6; Conservative 1; Mismatches 0; Indels
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118 GGEQAGG 124
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Gaps

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Score 34; DB 2; Length 266; Pred. No. 70; 1; Mismatches 1; Indels

81.0%; 75.0%;

Query Match
Best Local Similarity 75.0
Matches 6; Conservative

Search completed: September 18, 2004, 04:30:50 Job time : 11.7255 secs

193 LGGTKAGG 200

1 IGGEKAGG 8

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

September 18, 2004, 03:48:54; Search time 5.96078 Seconds (without alignments) 69.884 Million cell updates/sec

US-10-615-959-40 42 1 IGGEKAGG 8 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	cion	homo sapien		mus musculu	escherichia	zea mays (m	methanobact	methanobact	alcaligenes	schizosacch	streptomyce	herpes simp	thermoplasm	vibrio para	vibrio vuln	methanosarc	craterostiq	methanobact	caulobacter	homo sapien	mus musculu	rattus norv	neisseria m	neisseria m	vibrio chol	drosophila	streptomyce	deinococcus	bacillus su	homo sapien	rattus norv	cyprinus ca	lumbricus r	homo sapien
	Description	P02461		_	-		027600	059579									_					. ,				09vyq5 (							046157 ]	
SUMMARIES	ID	CA13 HUMAN	CA13_RAT	CA13 MOUSE	YJHT ECOLI	HS21_MAIZE	FWDC_METTH	FWDC_METTM	MERA_ALCSP	RL12_SCHPO	YGL2_STRVR	RIRI_HSV11	YD63_THEAC	TRMU_VIBPA	TRMU_VIBVU	DP2L_METAC	DHB CRAPL	FWDC_METWO	YX21_CAUCR	RL6_HUMAN	RL6_MOUSE	RLG_RAT	HSLO_NEIMA	HSLO_NEIMB	YH74_VIBCH	C318_DROME	FISK_STRCO	YT93_DEIRA	XKDO_BACSU		m`	UR1_CYPCA	RL13_LUMRU	RB2A_HUMAN
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## ALIGNMENTS

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Ramirez F.;
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Chu M.-L., Weil D., de Wet W.J., Bernard M.P., Sippola M., Ramirez F
"Isolation of cDNA and genomic clones encoding human pro-alpha 1
(III) collagen. Partial characterization of the 3' end region of the
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"Nucleotide sequence of a cDNA coding for the amino-terminal region of human prepro alpha 1(III) collagen.";
Nucleic Acids Res. 16:7201-7201(1998).
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MEDLINE-93293988; PubMed-8514866;
Tromp G., Wu Y., Prockop D.J., Madhatheri S.L., Kleinert C.,
Earley J.J., Zhuang J., Noerrgaard O., Darling R.C., Abbott W.M.,
Cole C.W., Jaakkola P., Ryynaenen M., Pearce W.H., Yao J.S.T.,
Majamaa K., Smullens S.N., Gatalica Z., Ferrell R.E., Jimenez S.A.,
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                                                                                                                                                                                                         Rosenbloom J., Myers J.C.; "Molecular cloning and carboxyl-propeptide analysis of human type
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SEQUENCE OF 950-1466 FROM N.A.
MEDIINE=88189827; PubMed=3357782;
Mankoo B.S., Dalgleish R.;
"Human pro alpha 1(III) collagen: cDNA sequence for the 3' end.";
Nucleic Acids Res. 16:2337-2337(1988).
                                                                                                                Molyneux K., Dalgleish R.; "Human type III collagen 'variant' is a cDNA cloning artefact."; Nucleic Acids Res. 16:11833-11833 (1988).
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MEDLINE=89378725; PubMed=2777083;
Benson-Chanda V., Su M.W., Weil D., Chu M.-L., Ramirez F.;
"Cloning and analysis of the S' portion of the human type-III
                                                                                                                                                                                                                                                                                MEDIINE=81208139; PubMed=7016180;
Seyer J.M., Kang A.H.;
"Covalent structure of collagen: amino acid sequence of alpha
                                                                                                                                                                                        Loidl H.R., Brinker J.M., May M., Pihlajaniemi T., Morrow S.,
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Miskulin M., Dalgleish R., Kluve-Beckerman B., Rennard S.I.,
Tolstoshev P., Brantly M., Crystal R.G.;
"Human type III collagen gene expression is coordinately mod
with the type I collagen genes during fibroblast growth.";
Biochemistry 25:1408-1413(1986).
                                                                                                                                                                                                                                                                                                                       1(III)-CB9 from type III collagen of human liver."; Biochemistry 20:2621-2627(1981).
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                                                                                                                                                                   SEQUENCE OF 1065-1466 FROM N.A.
MEDLINE=85087944; PubMed=6096827;
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MEDLINE=88303360; PubMed=3405773;
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Gene 78:255-265(1989).
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MEDLINE=91056145; PubMed=2243125;
Kontusaari S., Tromp G., Kuivaniemi H., Romanic A.M., Prockop D.J.;
"A mutation in the gene for type III procollagen (COL3A1) in a family
                                             mutations
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Tromp G., Kuivaniemi H., Stolle C.A., Pope F.M., Prockop D.J.;
"Single base mutation in the type III procollagen gene that converts
the codon for glycine 881 to aspartate in a mild variant of
Ehlers-Danlos syndrome IV.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acid
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MEDILINE-89109135; PubMed=2492273;

MEDILINE-89109135; PubMed=2492273;

"A single base mutation that substitutes serine for glycine 790 of the alpha i (III) chain of type III procollagen exposes an arginine and causes Ehlers-Danlos syndrome IV.";

J. Biol. Chem. 264:1349-1352(1989).
                                                                                                                                                                                                                                                                  MEDLINE=91045136; PubMed=2235526; Zafarullah K., Kleinert C., Tromp G., Kuivaniemi H., Kontusaari S., Wu Y., Ganguly A., Prockop D.J.; Tromp G., Apolymorphism in exon 31 of the COL3Al gene."; Nucleic Acids Res. 18:6180-6180(1990).
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III collagen
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Richards A.J., Ward P.N., Narcisi P., Nicholls A.C., Lloyd J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-55268429; PubMed-7749417;
Tromp G., de Paepe A., Nuytinck L., Madhatheri S.L., Kuivaniemi
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Ehlers-Danlos syndrome type IV.";
Hum. Mutat. 5:179-181(1995).
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Richards A.J., Lloyd J.C., Ward P.N., de Paepe A., Narcisi P.,
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Johnson P.H., Richards A.J., Pope F.M., Hopkinson D.A.;
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                                                                                                                                                           J. Clin. Invest. 91:2539-2545(1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: Collagen type III occurs in most soft connective tissues along with type I collagen.
-!- SUBUNT: Trimers of identical alpha 1(III) chains. The chains are linked to each other by interchain disulfide bonds. Trimers are also cross-linked via hydroxylysines.
-!- PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94114571; PubMed=8286415; Glumoff V., Maekelae J.K., Vuorio E.; Clumoff V., Maekelae J.K., Vuorio E.; "Cloning of cDNA for rat pro alpha 1(III) collagen mRNA. Different expression patterns of type I and type III collagen and fibronectin genes in experimental granulation tissue."; Biochim. Biophys. Acta 1217:41-48(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE OF 308-482 FROM N.A.
MEDLINE=88256083; PubMed=2456904;
Frankel F.R. Hav C.-Y.J., Meyers J.C., Lin E., Lyttle C.R.,
Komm B., Mohn K.;
Komm B., Mohn K.;
Mrsgulation of alpha 2(I), alpha 1(III), and alpha 2(V) collagen
mRNAs by estradiol in the immature rat uterus.";
DNA 7:347-354(1988).
                                        ö
   DB 1; Length 1466;
                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 73-636 FROM N.A.
STRAIN=Sprague-Dawley; TISSUE=Fibroblast;
Wurtz T., Ellerstroem C., Lundmark C., Christersson C.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                      P13941; 070604;
01-JAN-1990 (Rel. 13, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Score 42; DB 1
Pred. No. 5.6;
                                      0; Mismatches
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COL3A1.
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EMBL; AJ005395; CAA66510.1; --
EMBL; AJ1364; AAA40942.1; --
PIR, S41067; S41067.
InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
InterPro; IPR008181; Fib_collagen.
InterPro; IPR0011007; VWFC.
Pfam; PF01391; Collagen, 6.
Probom; PD00007; Clg helix; 1.
Probom; PD002078; Fib_collagen_C.
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Best Local Similarity
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Gaps
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"The mouse type-III procollagen-encoding gene: genomic cloning and
complete DNA sequence.";
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
          PROSITE; PS01208; VWFC 1; PARTIAL.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
Collagen; Glycoprotein.
                                                                                                                                                              ;
0
                                             COLLAGEN ALPHA 1(III) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE.
TRIPLE-HELICAL REGION.
NONHELICAL REGION (C-TERMINAL).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                          Score 38; DB 1; Length 636;
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                                                                                                                        61A48159F01D01EE CRC64;
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                                                                                                                                                                                                                                            CARL MOUSE STANDARD, PRT; 1464 AA. P08121; Q61429; Q9CRN7, 01-AUG-1988 (Rel. 08, Created) 15-UL-1999 (Rel. 38, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Collagen alpha 1(III) chain precursor.
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A -> G (IN REF
                                                                                                                                                   Pred. No. 14;
2; Mismatches
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STRAIN=C57BL/6 X DBA; TISSUE=Embryo;
MEDLINE=95011609; PubMed=7926795;
SMART; SM00038; COLFI; 1.
PROSITE; PS01208; VWFC_1; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-488 FROM N.A.
MEDLINE=88167858; PubMed=3443309;
Wood L., Theriault N., Vogeli G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human and mouse cDNA sequences
                                                                                                                        62332 MW;
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InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
InterPro; IPR008181; Fib_Collagen.
InterPro; IPR00181; Fibrinogen.C.
InterPro; IPR001007; WWF.C.
Pfam; PF01410; COLFI; 1.
Pfam; PF01391; Collagen; 18.
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859 859
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                                                                                                                                                                                                                                                                                               Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YJHT ECOLI
P39371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
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                                                                                                                                                                                                                                             C STRAIN-CSTBL/GG1; TISSUE=Embryonic head;

XA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Xawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Xaharawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A lazawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Xaito T., Okazaki Y., Gojobori T., Bono H., Xasukawa T., Saito R.,

Xa dito T., Okazaki Y., Giosi C., King B., Kochiwa H.,

Xa kadota K., Matsuda H.A., Ashburner M., Batalov S., Gasavant T.,

Xa kadota K., Matsuda H.A., Ashburner M., Batalov B., Kochiwa H.,

Xa kuhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

A Urons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Assaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Xa Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Havachiyaki V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         collagen mRNAs.";
Biochim. Biophys. Acta 1089:241-243(1991).
-!- FUNCTION: Collagen type III occurs in most soft connective tissues along with type I collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: O-linked glycan consists of a Glc-Gal disaccharide bound to the oxygen atom of a post-translationally added hydroxyl group (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBJUNT: Trimers of identical alpha 1(III) chains. The chains are linked to each other by interchain disulfide bonds. Trimers are also cross-linked via hydroxylyaines.

PTM: Proline residues at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the
  "Complete nucleotide sequence of the N-terminal domains of the murine alpha-1 type-111 collagen chain.";
                                                                                                           MEDLINE-85131189; PubMed=3972847;
Liau G., Mudryj M., de Crombrugghe B.;
"Identification of the promoter and first exon of the mouse alpha 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91274355; PubMed=2054384;
Metsaeranta M., Toman D., de Crombrugghe B., Vuorio E.;
"Specific hybridization probes for mouse type I, II, III and IX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Contains 1 VWFC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; KU3037; -; NTTANUTATED_CDS.
EMBL; AK019448; BAB31724.1; -.
EMBL; K57983; CAA41048.1; -.
PIR; AZ7353; AZ7353.
PIR; S59856; S59856.
MGD; MGI:884422.
                                                                                                                                                                          [1] collagen gene.";
Biol. Chem. 260:3773-3777(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1442-1464 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X52046; CAA36279.1; -.
EMBL; BC043089; AAH43089.1; -.
EMBL; BC058724; AAH58724.1; -.
                                                                                                                                                                                                                                      SEQUENCE OF 810-1464 FROM N.A.
                                                                                          SEQUENCE OF 1-28 FROM N.A.
                                                 Gene 61:225-230(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8 through 100 minutes."; Nucleic Acide Res. 23:2105-2119 (1995).
-! SIMILARITY: Contains 7 Kelch repeats.
-! SIMILARITY: STRONG, TO H.INFLUENZAE H10148.
Probom; PD000007; Clg helix; 1.
Probom; PD002078; Fib_collagen_C; 1.
SMART; SM0014; VWC; 1.
SMART; SM00214; VWC; 1.
PROSITE; PS01208; WFC 1; 1.
PROSITE; PS50184; VWFC 2; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
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WONHELICAL REGION (N-TERMINAL).

TRIPLE-HELICAL REGION (TERMINAL).

NONHELICAL REGION (TERMINAL).

O-LINKED (GAL. . .) (BY SIMILARITY.

HYDROXYLATION (BY SIMILARITY).

HYDROXYLATION (BY SIMILARITY).

HYDROXYLATION (BY SIMILARITY).

HYDROXYLATION (BY SIMILARITY).

HYDROXYLATION (BY SIMILARITY).

HYDROXYLATION (BY SIMILARITY).

HYDROXYLATION (BY SIMILARITY).

INTERCHAIN (BY SIMILARITY).

INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB 1; Length 1464;
                                                                                                                                                                                                                                                                               AMINO-TERMINAL PROPEPTIDE.
COLLAGEN ALPHA 1(III) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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STRAIN=K12 / MG1655;
MEDLINE=99334362; PubMed=7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein yjhT precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 368 AA.
                                                                                                                                                                                                  matrix, Collagen; Signal.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 31;
2; Mismatches
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                         EMBL; U14003; AAA97206.1; ALT INIT.
EMBL; AE000501; AAC77266.1; ALT_INIT.
ECOGENE; EG12562; A)hT.
INTERPRO, IPRO06652; Kelch_rep.
Pfam; PF01344; Kelch; 2.
Hypothetical protein; Kelch repeat; Repeat; Signal; Complete proteome.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=cv. Ohio 43; TISSUB=Radicle;
MEDLINE=91329703; PubMed=114312;
MEDLINE=91329703; PubMed=114312;
Goping 1.S., Frappier J.R.H., Malden D.B., Atkinson B.G.;
"Sequence, identification and characterization of cDNAs encoding two different members of the 18 kDa heat shock family of Zea mays L.";
Plant Mol. Biol. 16.699-711(1991).
-!- SUMCELLUIAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the small heat shock protein (HSP20)
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILÀRITY: PLANTS HAVE FOUR CLASSES OF HSP20: CLASS I AND II WHICH ARE CYTOPLASMIC; CLASS III WHICH IS IN THE CHLOROPLAST AND CLASS IV WHICH IS IN THE ENDOMEMBRANE. THIS PROTEIN BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                     ..
0
                                                                                                                                                                                                                                                                                                       Score 36; DB 1; Length 368;
                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                         1194F392C51EA204 CRC64;
                                                                                                                                                  HYPOTHETICAL PROTEIN YJHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR.1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-UUN-1994 (Rel. 29, Last annotation update)
17.5 kDa class II heat shock protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 AA.
                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                      Pred. No. 19;
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KELCH 5.
                                                                                                                                                                 KELCH 1.
KELCH 2.
KELCH 3.
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InterPro; IPR008978; HSP20_chap.
                                                                                                                                                                                                                                                                         39572 MW;
                                                                                                                                                                                                                                                                                                     85.7%;
                                                                                                                                                                                                                                                                                                                      87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00011; HSP20; 1. TROSITE; PS01031; HSP20; 1.
                                                                                                                                                                                                                                                                                                                   Local Similarity 87.5
1es 7; Conservative
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137
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                                                                                                                                                                                                                                                                                                                                                                 1 IGGEKAGG 8
                                                                                                                                                                                                                                                                         368 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4577;
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86
139
174
222
287
338
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P24631;
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30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Tungsten-containing formylmethanofuran dehydrogenase II subunit
                                                ..
                                                                                                                                                                                                                      Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.
                             Length 161;
Heat shock; Multigene family.
SEQUENCE 161 AA; 17511 MW; 3E60A8DD4396577C CRC64;
                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the fwdC/fmdC family.
                           Score 35; DB 1;
Pred. No. 13;
1; Mismatches
                          th 83.3%; Score 35; Similarity 85.7%; Pred. No. 36; Conservative 1; Mismatch
                                                                                                                                                                                                              Methanobacterium thermoautotrophicum.
                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000916; AAB86032.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; H69074; H69074.
InterPro; IPR002489; DUF14.
                                                                                                                                   STANDARD;
                                                                               30 GGDKAGG 36
                                    Local Similarity
                                                                  2 GGEKAGG 8
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           NCBI_TaxID=187420;
                                                                                                                                                                                            (EC 1.2.99.5).
FWDC OR MTH1558.
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                           Query Match
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: Methanogenesis; first step.
SUBUNIT: THIS ENZYME IS COMPOSED OF SEVEN SUBUNITS FWDA (65 kDa), FWDB (53 kDa), FWDC (31 kDa), FWDD (15 kDa), FWDE, FWDF, AND FWDG (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DI Serre...

EMBL; X87970; CAA61214.1; -.

InterPro; IPR002489; DUF14.

Pfam; PF01493; GXGXG; 1.

Pram; PF01493; GXGXG; 1.

Pram; PF01493; GXGXG; 1.

Pram; PF01493; CXCXG; 1.

Pram; PF01493; CXCXG; 1.

Pram; PF01493; CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CXCXC, CX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDUCTION: By growth on tungsten or molybdenum under anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Tungsten-containing formylmethanofuran dehydrogenase II subunit C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133)
                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea, Buryarchaeota, Methanobacteria, Methanobacteriales,
Methanobacteriaceae, Methanothermobacter.
                                                                                                                        83.3%; Score 35; DB 1; Length 270; 75.0%; Pred. No. 22; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E0A369D2ACFEC46F CRC64;
175 5.
194 6.
213 7.
28641 MW; 043A9FFBBA554D36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Belongs to the fwdC/fmdC family.
                                                                                                                                                                                                                                                                                                                                                                                                               270 AA
                                                                                                                                                                                                                                                                                                                                                                                                               FWDC_METTM STANDARD; E
Q59579; 0008493;
30-MAY-2000 (Rel. 39; Created)
30-MAY-2000 (Rel. 39; Last sequ
30-MAY-2000 (Rel. 39; Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28554 MW;
                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COFACTOR: Tungsten.
                                                                                                                                                                                                                                                                                    200 VGGEMAGG 207
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163
182
201
270 AA;
163 1
182 1
201 2
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                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
                                                                                                                                                                                                                                 1 IGGEKAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=79929;
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99
118
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REPEAT
REPEAT
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FWDC_METTM
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Matches
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                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nikiforov V., Yurieva O., Kholodii G., Minakhin L., Gorlenko Z. Kalyaeva E., Mindlin S., Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Alcaligenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oxidoreductase; Flavoprotein; FAD; NADP; center; Metal-binding; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FAD (ADP PART) (BY SIMILARITY)
  Score 35; DB 1; Length 270; Pred. No. 22;
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0603DDD6B13CB519 CRC64;
                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Mercuric reductase (EC 1.16.1.1) (Hg(II) reductase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REDOX-ACTIVE.
MERCURY (POTENTIAL).
MERCURY (POTENTIAL).
                                                 1;
                                                                                                                                                                                                                                                       559 AA
                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! - SIMILARITY: Contains 1 HMA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00076; PYRIDINE_REDOX_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR001327; FAD_pyr_redox.
Interpro; IPR006121; HeavyMe_transpt.
Interpro; IPR008131; HeavyMe_transpt.
Interpro; IPR008191; Metal_bind.
Interpro; IPR001100; Pyr_redox.
Interpro; IPR004099; pyr_redox_dim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000139; FAD pyr redox; 1. PROSITE; PS01047; HMA 1; 1. PROSITE; PS50846; HMA 2; 1.
                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00070; pyr_redox; 1.
Pfam; PF02852; pyr_redox_dim; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58019 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Y08993; CAA70190.1; -. HSSP; Q04656; 1AW0.
  similarity 75.0%; 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00368; FADPNR.
PRINTS; PR00945; HGRDTASE.
PRINTS; PR00411; PNDRDTASEI.
                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                           Alcaligenes sp.
Plasmid IncHI2 pMER610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Redox-active
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                                                                                                                                      200 VĠĠĖMÄĠĠ 207
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556
557
559 AA;
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Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                              1 IGGEKAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=512;
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InterPro; IPR000911; Ribosomal\_L11.

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Mood V. Gwilliam R., Rajandram M.A., Lyne M., Lyne R., Stewart A., Mood V., Gwilliam R., Baker S., Basham D., Bowman S., Bachors J., Baker S., Basham D., Bowman S., Chillingworth T., Churcher C.M., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Gobner R., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Bornaby T., Howarth S., Huckle E.J., Hunt S., Jagels K., Jones L., Jones M., Leather S., McDonald S., Midcan J., Noney E., Noule S., Mungall K., Murphy L., Nibbett D., Odell C., Anoney P., Moule S., Mungall K., Murphy L., Nibbett D., Odell C., Antherford K., Rutter S., Saunders R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Relton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Berr M., Canger I., Berk A., Lehrach H., Reinhardt R., Pohl T.M., Berzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Potts S.M., Losan M., Rochet M., Gallardin C., Moore K., Hurst S.M., Losan M., Rochet M., Gallardin C., Moreno S., Armstrong J., Forsburg S.L., Lowe T., Jimenez J., Sanchez M., Garzon A., Thode G., Bominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., Moreno S., Armstrong J., Prossburg S.L., The genome sequence of Schizosaccharomyces pombe.";

Nature 41:871-880 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as a since content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: This protein binds directly to 26S ribosomal RNA (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- MISCELLANEOUS: There are two genes for L12 in S.pombe.
-!- SIMILARITY: Belongs to the L11P family of ribosomal proteins.
                                                   ;
  Score 35; DB 1; Length 559;
Pred. No. 44;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
60S ribosomal protein 112.
(RPL12A OR SPCG31H12.04C) AND (RPL12B OR SPCC1H12.04C) AND (RPL12B OR SPCC1H2.04C) AND (BAL12B OR SPCCH6C4.13C).
Schizosaccharomyces pombe (Fissaion yeast).
Eukaryota, Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetaes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (RPL12A AND RPL12B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL031824; CAA21221.1; -. EMBL; AL031535; CAA20752.1; -. PIR; T41103; T41103.
  83.3%;
                                              6; Conservative
                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces.
                                                                                                                  ||:||||
87 GGDKAGG 93
Query Match
Best Local Similarity
                                                                                           2 GGEKAGG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4896
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                                                                                                                                                                                                                                                   SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=972;
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ID _RL12_S
                                            Matches
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GeneDB\_SPombe; SPCC16C4.13c; -.
GeneDB\_SPombe; SPCC31H12.04c; -.

HSSP; P29395; 1MMS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Behrmann I., Hillemann D., Puehler A., Strauch E., Wohlleben W.; "Overexpression of a Streptomyces viridochromogenes gene (glnII) encoding a glutamine synthetase similar to those of eucaryotes confers resistance against the antibiotic phosphinothricyl-alanyl-alanine."; J. Bacteriol. 172:5326-5334(1990).
                                                                                                                                                                           Gaps
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01-MAR-1989 (Rel. 10, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Ribonucleoside-diphosphate reductase large chain (EC 1.17.4.1)
(Ribonucleotide reductase) (136 kDa subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                     81.0%; Score 34; DB 1; Length 240; 85.7%; Pred. No. 30; ive 1; Mismatches 0; Indels
                                                               PROSITE; PS00359; RIBOSOMAL L11; 1.
Ribosomal protein; RNA-binding; Multigene family.
SEQUENCE 165 AA; 17666 MW; FC777B46CD08F005 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 AA; 23914 MW; 09DB6BEE681F7E2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 23.9 kDa protein in glnII region (ORF2).
Streptomyces viridochromogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1137 AA.
                                                                                                                                                                                                                                                                                                                                   PRT;
              Pfam; PF03946; Ribosomal L11; I. Pfam; PF03946; Ribosomal L11 N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90368592; PubMed=1975583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X52842; CAA37027.1; -. PIR; B36724; B36724.
Hypothetical protein.
                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.73
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                 SMART; SM00649; RL11;
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18 VGGEVAGG 25
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                                                                                                                                                    Best Local Similarity
Matches 6: Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                            1 IGGEKAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1938;
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P19435;
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                                                                                                                                       Query Match
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RIR1_HSV11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
(BC 2.1.1.61).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=RIMD 2210633 / Serotype O3:K6;
MEDLINE=22508454; PubMed=12620739;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
genome sequence of the thermoacidophilic scavenger Thermoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·,
                                                                                                                                      -i- SIMILARITY: Contains 1 HTH cro/C1-type DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01381; HTH 3; 1.
SWART; SM00530; HTH XRB; 1.
PROSITE; PS50943; HTH CROC1; 1.
Hypothetical protein; Transcription regulation; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vibrio parahaemolyticus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 1; Length 312;
Pred. No. 59;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 163 H-T-H MOTIF (POTENTIAL).
312 AA; 35272 MW; A0EC3FF0B3D72662 CRC64;
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    -!- SUBCELLUIAR LOCATION: Cytoplasmic (By s
    -!- SIMILARITY: Belongs to the trmU family.

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87.5%;
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InterPro; IPR001387; HTH 3.
                                                                                                  Nature 407:508-513(2000).
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Best Local Similarity
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McGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,
McNab D., Perry L.J., Soctt J.B., Taylor P.;
"The complete DNA sequence of the long unique region in the genome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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MEDLINE=20479972; PubMed=11029001;
MEDLINE=20479972; Santos-Martinez M.-L., Koretke K.K., Volker C.,
Mevep A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PATHWAY: DNA replication pathway; first step.
SUBUNIT: Heterodimer of a large and a small chain.
SIMILARITY: Belongs to the ribonucleoside diphosphate reductase large chain family.
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15-MAR-2004 (Rel. 43, Last annotation update)
Putative HTH-type transcriptional regulatory protein Tal363
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Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR00188; Ribonucleo_red.

Pfam; PF00317; ribonuc_red_lg; 1.

PRIMIPS: PR01867; ribonuc_red_lgc; 1.

PRINTS; PR01818; RIBONETASEM!

PROSITE; PS00089; RIBONED_LARGE; 1.

Oxidoreductase; DNA replication; Barly protein.

CONFLICT 70 70 N -> S (IN REF. 2).

CONFLICT 1034 1034 A -> P (IN REF. 2).

SEQUENCE 1137 AA; 124050 MW; 8A31777F4C22D8F85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           herpes simplex virus type 1.";
J. Gen. Virol. 69:1531-1574(1988)
                          Alphaherpesvirinae; Simplexvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
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les 5; Conservative
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                                                                       NCBI_TaxID=10299;
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TA1363. RESULT 12
YD63\_THEAC
ID 28-FE
DT 28-FE
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Matches

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Gaps

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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA polymerase II large subunit (EC 2.7.7.7) (Pol II)
CC OR MA4552.
       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifised and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch).ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-homocysteine + tRNA containing 5-methylaminomethyl-2-
                                                                                                                                                                                                                                                                               10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
(BC 21.1.61)
TRMU OR VU12926.
Vibrio vulnificus.
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF_00144; -; 1.
InterPro; IPR004566; TrmU.
Pfam; PF03054; tRNA Me_trans; 1.
IIGRFAMS; TIGR00420; trmU; 1.
ITGRFAMS; TIGR00420; trmU; 1.
Transferase; Methyltransferase; tRNA processing; Complete proteome.
SEQUENCE 374 AA; 42138 MW; FS35AE8671826EEC CRC64;
HAMAP; MF_00144; -; 1.
InterPro; IRR04506; TrmU.
Pfam; PF03054; tRNA Me_trans; 1.
TIGRFAMS; TIGR0420; trmU; 1.
Transferase; Methyltransferase; tRNA processing; Complete proteome.
SEQUENCE 374 AA; 42198 MW; 5BA02165BD84D5B5 CRC64;
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Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                              Query Match 78.6%; Score 33; DB 1; Length 374; Best Local Similarity 75.0%; Pred. No. 70; Matches 6; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.6%; Score 33; DB 1; Length 374; 75.0%; Pred. No. 70; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thiouridylate.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the trmU family.
                                                                                                                                                                                                                                                       374 AA.
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Best Local Similarity 75.0v
Best Local 6; Conservative
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                                                                                                                                                                                 251 iĠĠŖĶĠĠĠ 258
                                                                                                                                                       1 IGGEKAGG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                   TRMU VIBVU
Q8CWJ6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P., FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A., Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R., Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W., Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M., Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A., Liu M., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario B.C., Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I., Mctchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E., Metcalf W.W., Birren B.;

"The genome of Methanosarcina acetivorans reveals extensive metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase; DNA-directed DNA polymerase; DNA replication; Hydrolase; Nuclease; Environmentase; DNA-binding; Multifunctional enzyme; SEQUENCE 1145 AA: 127479 MM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphates.
-!- SUBUNIT: Heterodimer of a large subunit and a small subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: Belongs to the archaeal DNA polymerase II family.
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                                 Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales; Methanosarcinaceae; Methanosarcina.
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                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=C2A / ATCC 35395 / DSM 2834;
MEDLINE=21929760; PubMed=11932238;
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InterPro; IPR004475; PolC DP2.
Pfam; PF03833; PolC DP2; 1.
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Methanosarcina acetivorans
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Matches 6; Conservative
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                                                                                                  NCBI_TaxID=2214;
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Search completed: September 18, 2004, 04:26:21

Job time : 7.96078 secs

PRT; 1145 AA.

STANDARD;

DP2L\_METAC ID DP2L\_METAC AC Q8THG5;

AC AC

RESULT 15

251 IGGRKGGG 258

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1 IGGEKAGG 8

28-FEB-2003 (Rel. 41, Created)

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Gaps

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Q8n6u4 homo sapien

Q8px10 methanosarc

Q8bju6 mus musculu

Q8slv9 oryza sativ

Q7xpp9 oryza sativ

Q8k13 mus musculu

Q8k13 mus musculu

Q8bky2 mus musculu

Q8bky2 mus musculu

Q8bix4 mus musculu

Q8bix4 mus musculu

Q7tt32 mus musculu

Q7tt32 mus musculu

Q81i8 salmonella

Q15729 entamoeba h

Q62i8 salmonella

Q15729 entamoeba h

Q62i8 streptomyce

Q82r45 streptomyce
                                                                                                                                                  September 18, 2004, 04:00:08; Search time 28.3922 Seconds (without alignments) 88.903 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Q8BJU6
Q8S1V9
Q7WY41
Q7YP9
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Q8BLW4
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Gapop 10.0 , Gapext 0.5
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                                                                                                    - protein search, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length: 0
length: 2000000000
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Maximum DB seq
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Q8x554 escherichia Q8cvg5 escherichia Q8cvg5 escherichia Q8cvg5 escherichia E1 Q88930 pseudomonas Q7te92 canine coro Q7te92 canine coro Q92q09 rhizobium Q8x104 pseudomonas Q8x104 pseudomonas Q8x104 prochloroco Q7v317 prochloroco Q7v317 prochloroco Q7v317 prochloroco Q7v316 gamma proche	002129 drosophila 09v746 drosophila 066951 feline infe 096679 feromyloce 09ftt5 oryza sativ 089937 thauera aro 089203 medicago tr 07v0x9 oryza sativ 07xbq oryza sativ 09s202 medicago tr 07xbq oryza sativ 09s202 medicago tr 08s202 medicago tr 08s202 medicago tr 08s202 medicago tr 08s202 medicago tr 08s202 medicago tr 08s202 medicago tr 08s202 medicago tr 08s202 medicago tr 08s202 medicago tr 08s202 medicago tr 08s202 medicago tr
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## ALIGNMENTS

<pre>syndrome type tteleostomi; lomo. is. itituent; IEA.</pre>		163;
1.1  OBNGU4 PRELIMINARY; PRT; 1163 AA.  OBNGU4;  OLOCT-2002 (TrEMBLrel. 22, Last sequence update)  OL-OCT-2003 (TrEMBLrel. 25, Last sequence update)  OLOCT-2003 (TrEMBLrel. 25, Last annotation update)  OLOCT-2003 (TrEMBLrel. 25, Last annotation update)  OLOCT-2003 (TrEMBLrel. 25, Last annotation update)  Similar to collagen, type III, alpha 1 (Ehlers-Danlos syndrome ty  Home sapiens (Human).  Wentersomal dominant).  Benkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Wenmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  ILI TAXID=5606;  ILI TAXID=5606;  ILI SERUECE FROM N.A.  SEQUENCE FROM N.A.  Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.  Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.  SUBMBLS (Collagen) IEA.  OCOSENIS: Pettracollular matrix structural constituent; IE InterPro; IPRO01081; Fib. collagen. C.  InterPro; IPRO01081; Fib. collagen. C.  InterPro; IPRO01081; VWF-C.  Ffam; PFO1391; Collagen. C.  Ffam; PFO1391; Collagen. C.  Ffam; PFO1391; Collagen. C.  Ffam; PFO1391; VWF-C.  Frompon; PD002078; Fib. collagen. C.  Frompon; PD002078; Fib. collagen. C.  Frompon; PD002078; Fib. collagen. C.  Frompon; PD002078; Fib. collagen. C.  Frompon; PD002078; Fib. collagen. C.  Frompon; PD002078; Fib. collagen. C.  Frompon; PD002078; Fib. collagen. C.  Frompon; PD002078; Fib. collagen. C.  Frompon; PD002078; Fib. collagen. C.  Frompon; PD002078; Fib. collagen. C.  Frompon; PD002078; Fib. collagen. C.  Frompon; PD002078; Fib. collagen. C.  Frompon; PD002078; Fib. collagen. C.  Frompon; PD002078; Fib. collagen. C.  Frompon; PD002078; Fib. collagen. C.	9E0C6BE1E94D6357 CRC64;	DB 4; Length 1163; 53; 0. Indels
PRT; 1163 AA.  22, Created) 22, Last sequence update) 25, Last sequence update) 26, Last annocation update 26, Last annocation update 27, Last annocation update 28, Last annocation update 21, Last annocation update 22, Last annocation update 22, Last annocation update 23, Last annocation update 24, Last annocation update 25, Last annocation update 26, Last annocation update 26, Last annocation update 27, Last annocation update 28, Last annocation update 29, Last annocation update 21, Last annocation update 21, Last annocation update 22, Last annocation update 24, Last annocation update 25, Last annocation up		Score 42; Pred. No.
T.1  QBNGU4 PRELIMINARY; PRT; 1163 AA.  QBNGU4;  QBNGU4;  QBNGU4;  QBNGU4;  QBNGU4;  QBNGU4;  QBNGU4;  QBNGU4;  QBNGU4;  QBNGU4;  QBNGU4;  QBNGU4;  QBCT-2002 (TrEMBLrel. 22, Last sequence update)  QBCT-2002 (TrEMBLrel. 25, Last sequence update)  GBCT-2002 (TrEMBLrel. 25, Last sequence update)  Similar to collagen, type III, alpha 1 (Ehlers-Danlos s;  Similar to collagen, type III, alpha 1 (Ehlers-Danlos s;  Similar to collagen, type III, alpha 1 (Ehlers-Danlos s;  BUNARYOCA; Metazoa; Chordata; Craniata; Vertebrata; Euthomosapiens (Human)  BUNCH TAXID=9606;  [1]  TISSUBLIA TAXID=9606;  SEQUENCE FROM N.A.  SEGUENCE FROM N.A.  SETTAUB-9606;  STATUS BCO2819; FISACE COLLAGEN.  GG; GG: 0005581; C:collagen; IEA.  GG; GG: 0005581; C:collagen; IEA.  GG; GG: 0005581; C:collagen. C.  InterPro; IPRO0180; Pib. collagen. C.  InterPro; IPRO01007; VWF_C.  PÉAM; PFOL191; COLFI; 1.  PROD11; SMART; SM00014; VWFC. 1:  SMART; SM00014; VWFC. 1:  SMART; ENGOROFS; Eib. collagen. C; 1.  SMART; ENGOROFS; VWFC. 1:  SMART; SM00014; VWFC. 1:  PROSTITE: PSOLJOR; VWFC. 1:  PROSTITE: PSOLJOR; VWFC. 1:	PS50184; VWFC_2; 1. 1163 AA; 111899 MW;	100.0%; 100.0%;
LIT 1  OBN6U4  PRELIMINARY, OBN8U4; O1-OCT-2002 (TERMELEE). 2 O1-OCT-2003 (TERMELEE). 2 Similar to collagen, type Similar to collagen, type Similar to collagen, type IV, autosomal dominant). How sapiens (Human). How sapiens (Human).  HOWEN TAXID=9606; IN] TAXID=9606; IN] SEQUENCE FROM N.A. TISSUE=1.ver; Submitted (APR-2002) to the STREAMENT STREAMENT STREAMENT. SUBMIL, BCO28178; AAH28178. GO; GO:0005201; F: EXERZEC INTERPO; IPR001007; VWF PEAM; PRO1391; COLFI; 1. PEAM; PRO1391; COLFI; 1. PEAM; PRO1391; COLFI; 1. PEAM; PRO1391; COLFI; 1. PEAM; PRO1391; COLFI; 1. PEODOM; PMO0318; Fib. COLFI; 1. PROSITE; PROSITE; 1. PROSITE; PROSITE; 1.	PROSITE; PS501 Collagen. SEQUENCE 116	Query Match Best Local Similarity
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Oryza sativa (japonica cultivar-group).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                               90.5%; Score 38; DB 11; Length 338; 75.0%; Pred. No. 77;
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003268; BAB89698.1; -.
                                                                                                                                                SEQUENCE 338 AA; 35813 MW; 15BE369D8690F37A CRC64;
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G0; G0:00161G1; F:beta-amylase activity; IEA.

G0; G0:000272; F:bubtilase activity; IEA.

G0; G0:0000272; P:polysaccharide catabolism; IEA.

G0; G0:000508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR00154; Glyco hydro 14.

InterPro; IPR00209; Peptidase S8.

Pfam; PF01373; Glyco hydro 14; 2.

PROSITE; PS00136; SUBTIMSE ASP; 1.

SEQUENCE 415 AA; 46150 MW; 951DEBA6BDF2B7BA CRC6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative beta-amylase.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
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2; Mismatches
Pfam; PF01391; Collagen; 1.
ProDom; PD002078; Flb_collagen_C; 1.
SMART; SM00038; COLFI; 1.
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                       Query Match 90.5
Best Local Similarity 75.0
Matches 6; Conservative
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Q7WY41;
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Q8S1V9;
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STRAIN=C57BL/6J; TISSUE=Embryo;
STRAIN=22354683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
MANAYSIS of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=GOEL OF ROW N.A.

STRAIN=GOEL / GO1 / ATCC BAA-199 / DSM 3647 / OCM 88;

STRAIN=GOEL / GO1 / ATCC BAA-199 / DSM 3647 / OCM 88;

MEDLINE=22120827; PubMed=12125824;

Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,

Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C.,

Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,

Fritz H.-J., Gottschalk G.;

Fritz H.-J., Gottschalk G.;

Fritz H.-J., Gottschalk G.;

J. Mol. Microbiol Bacteria amazei: evidence for lateral gene

transfer between Bacteria and Archaea.";

J. Mol. Microbiol Biotechnol. 4:453-461(2002).
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MGD; MG: 18453; Collaal.
GO; GO:0005581; C:collagen; IEA.
GO; GO:0005581; F:excracellular matrix structural constituent; IEA.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Methanosarcina mazei (Methanosarcina frisia).
Archaea; Buryarchaeota; Euryarchaeota orders incertae sedis;
Methanosarcinales; Methanosarcinaceae; Methanosarcina.
NCBI_TaxID=2209;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
SEQUENCE 210 AA; 24264 MW; F53D2D1DB598AAF0 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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InterPro; IPR002181; Fibrinogen C.
InterPro; IPR000885; Fib_collagen_C.
Pfam; PF01410; CCLF1; I.
                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                 905 IGGEKAGG 912
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Best Local Similarity
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                      1 IGGEKAGG
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Q8PXL0;
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SEQUENCE 578L/60; TISSUE=Head;

MEDINE=22354683; PubMed=12466851;

The FANTOM Consortium.

A the RIKEN Genome Exploration Research Group Phase I & II Team;

"Analysis of the mouse transcriptome based on functional annotation of mouse transcriptome based on functional annotation of the following of the mouse transcriptome based on functional annotation of the following of the following in the following of the mouse transcriptome based on functional annotation of the following in the following in the following in the following in the following in the following in the following in the following in the following in the following in the following in the following in the following in the following in the following polonomy; Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonomy Polonom
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          GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                             Hypothetical protein; Collagen.
NON TER 1 1 1 SEQUENCE 1222 AA; 115140 MW; A409CA00D82765E4 CRC64;
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PROSITE; PS50184; VWFC_2; 1.
SEQUENCE 1464 AA; 138947 MW; 1E4ED9539EF42C12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1464 AA
                             InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
InterPro; IPR008180; Collagen.
InterPro; IPR000885; Fib_collagen.C.
Pfam; PF01410; COLFI; 1.
ProDom; PD000007; Clg helix; 1.
ProDom; PD000007; Clg helix; 1.
RNART; SM00038; COLFI 1.
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Best Local Similarity 75...
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Best Local Similarity 75.0
Matches 6; Conservative
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1206 VGGEKSGG 1213
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964 VGGEKSGG 971
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AL606645, CAR03516.1.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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He J., Rahme L.G.;
"Pseudomonas aeruginosa PA14 pathogenicity island (PAPI) 1.";
Submitted (APPT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY273869; AAP84143.1; -.
Hypothetical protein.
SEQUENCE 460 AA; 48289 MW; AS6F37B515F2F2BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.5%; Score 38; DB 10; Length 696; 100.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                  90.5%; Score 38; DB 2; Length 460; 75.0%; Pred. No. 1.1e+02; tive 2; Mismatches 0; Indels
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TISSUB-Breast tumor;
Strausberg R.;
Strausberg R.;
Submitted (AFR.2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC028248; AAH28248.1; -.
GO; GO:0005581; C:collagen; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
OSJNBAO055X19.24 protein.
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
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Best Local Similarity 75.0,
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                                                                                                                                                                                                                                                                                                                     Oryza sativa (Rice).
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SEQUENCE FROM N.A.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CS7BL/63; TISSUE=Aorta, and Vein;
MEDLINE=22354681; PubMed=12466851;
The FANTOM Consortium
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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STRAIN=C57BL/6; TISSUE-Brain;
STRAIN=2238B25; Dubmed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AK041115; BAC30826.1; -.
MGD; MG1:88453; COl3a1.
GO; GO:0005581; C:collagen; IEA.
InterPro; IPR008161; Clg_helix.
InterPro; IPR008161; Clg_helix.
InterPro; IPR008161; Clagaen.
InterPro; IPR008181; Fibrinogen.C.
InterPro; IPR00885; Fib.collagen.C.
InterPro; IPR001885; Fib.collagen.C.
InterPro; IPR0010885; Fib.collagen.C.
                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                 Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                      PRT; 1464 AA
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Pfam; PF01391; Collagen; 18.
ProDom; PD0000007; Clg_helix; 1.
ProDom; PD002078; Fib_collagen_C; 1.
SMART; SM00038; COLFI; 1.
                                                                                                                                   Created)
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
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nes 6, Conservative
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                                                                   PRELIMINARY;
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1206 VGGEKSGG 1213
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Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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                                                                   Q8BLW4
Q8BLW4;
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RESULT 9
Q8BLW4
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The state of a hemolysin and a vibrio species.";

"Cloning of a hemolysin encoding region of a Vibrio species.";

"Cloning of a hemolysin encoding region of a Vibrio species.";

"Cloning of a hemolysin encoding region of a Vibrio species.";

"Cloning of a hemolysin encoding region of a Vibrio species.";

"Cloning of a hemolysin course membrane (BY SIMILARITY).

"In SIMILARITY: BELONGS TO THE OMP25 / ROPB FAMILY.

"EMBL, AJ314791; CAC40971.1; -..

"RO): GO:0019867; C:external outer membrane (Sensu Gram-negativ. .; IEA.

"RO): GO:0019867; C:outer membrane; IEA.

"InterPro: IPR006665; OmpA/Moct."

"InterPro: IPR006498; OmpA/Moct."

"InterPro: IPR000498; OmpA/moct."

"Pfam; PF01691; OMPA-membrane; 1.

"PRINTS; PR01021; OMPA-MOCHS! 1.
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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Outer membrane protein).
Vibrio sp. CH-291.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.1%; Score 37; DB 2; Length 378; 75.0%; Pred. No. 1.3e+02; ive 1; Mismatches 1; Indels
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Strausberg R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC052398; AAH52398.1; -.
Hypothetical protein.
SEQUENCE 1464 AA; 138971 MW; 2B38BC27AF21590B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Antigen, Outer membrane.
SEQUENCE 378 AA; 40886 MW; ASESOFAC4D8814C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.
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Best Local Similarity 75.0
Matches 6; Conservative
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186 VGGEKTGG 193
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Best Local Similarity
Matches 6; Conserv
[2]
SEQUENCE FROM N.A.
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                                                                                                           SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=TY2 / Arcc 700931;
STRAIN=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laclette J.P., "Cloning, characterization and functional expression of a cyclophilin of Entamoeba histolytica."; Mol. Biochem. Parasitol. 107:219-225(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                     "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
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                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)

Cyclophilin (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

88.1%; Score 37; DB 16; Length 476;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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               082118 PRELIMINARY; PRT; 476 AA.
082118,
001-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 24, Last annotation update)
101-UN-2003 (TrEMBLrel. 24, Last annotation update)
5774577 OR 14274.
Salmonella typhi.
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                                                                                                                                                                                          MEDLINE=21534947; PubMed=11677608;
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NCBI_TaxID=5759;
                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 185:2330-2337(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20243663; PubMed=10779598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL627282; CAD09352.1; -. EMBL; AE016848; AA071732.1; -.
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211 VGGKKAGG 218
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                                                                                                                                           NCBI_TaxID=601;
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Matches
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COMEGA=0).

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LONGIAL ARCH7993; AAB86601.1; -.

DR EMBL, ARCH3993; AAB886601.1; -.

DR HSSP; POSO92; 2CPL.

COSO042027; F:cyclophilin-type peptidyl-prolyl cis-trans . . .; IEA.

BR GO; GO:0044600; F:cyclophilin; IEA.

COSO030051; F:FK506-sensitive peptidyl-prolyl cis-trans i. .; IEA.

BR GO; GO:001853; F:isomerase activity; IEA.

COSO030051; F:FK506-sensitive peptidyl-prolyl cis-trans i. .; IEA.

COSO030051; F:FK506-sensitive peptidyl-prolyl cis-trans i. .; IEA.

COSO030051; F:FK506-sensitive peptidyl-prolyl cis-trans i. .; IEA.

COSO030051; F:FK506-sensitive peptidyl-prolyl cis-trans i. .; IEA.

COSO030051; F:FK506-sensitive peptidyl-prolyl cis-trans i. .; IEA.

COSO030051; F:FK506-sensitive peptidyl-prolyl cis-trans i. .; IEA.

COSO030051; F:FK506-sensitive peptidyl-prolyl cis-trans i. .; IEA.

COSO030051; F:FK506-sensitive peptidyl-prolyl cis-trans i. .; IEA.

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Caballero-Franco C., Petrosyan P., Carrero-Sanchez J.C.,
De la Torre P., Laclette J.P., Ostoa-Saloma P.,
"Entamoeba histolyrica nucleotide sequence containing the gene for a
small heat shock protein, the CYP1 cyclophilin gene and a truncated
ORF for a putative serine/threonine protein kinase.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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-!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
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MEDLINE=97288094; PubMed=9143135;
Rathbone D.A., Holt P.J., Lowe C.R., Bruce N.C.;
"Molecular analysis of the Rhodococcus sp. strain HI her gene characterization of its product, a heroin esterase, expressed Escherichia coli.";
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Last annotation update)
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100.0%; Pred. No. 84;
ative 0; Mismatches
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GO; GO:0016787; F:hydrolase activity; IEA
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Hydrolase.
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01-JUL-1997 (TrEMBLrel,
01-OCT-2003 (TrEMBLrel,
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STRAIN=NA-4600 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
STRAIN=NA-4600 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
STRAIN=NA-4600 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
Ikeda H. Ishikawa J., Hanacto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S.;
"Complete genome sequence and comparative analysis of the industrial microorganism Streptonyces avermitilis.";
Nat. Biotechnol. 21:526-531(2003).
EMBL; AP005022; BAC68008.1; -..
GO; GO:0003824; F:catalytic activity; IEA.
InterPro; IPRO0379; Ser_estrs.
Complete proteome.
SEQUENCE 338 AA; 36242 MW; EA33486345FD82EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (1)
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NREL 8165;
MEDLINE=21477403; PubMed=11572948;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
metabolites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.7%; Score 36; DB 16; Length 338; 75.0%; Pred. No. 1.8e+02; rive 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                            01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative arylesterase/monoxygenase.
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Best Local Similarity 75.0
Matches 6; Conservative
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156 VGGESAGG 163
1 IGGEKAGG 8
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Search completed: September 18, 2004, 04:29:37 Job time : 31.3922 secs

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US-10-615-959-41 48 Title: Perfect score:

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Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1586107 seqs, 282547505 residues Searched: Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 2000000000 Minimum | Maximum |

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq\_29Jan04:\*
1: geneseqp1990s:\*
2: geneseqp1990s:\*
4: geneseqp2001s:\*
5: geneseqp201s:\*
6: geneseqp2033s:\*
7: geneseqp2033s:\* geneseqp2004s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Aab61741 Human typ	Aab61743 Human typ	Human	Aar92068 Recombina		Aay07375 Procollad	Abu70813 Human adi	Aau23675 Novel hum	Human	Abg61719 Novel ova		Aaw12843 Pro-alpha	Aaw12842 Truncated	Ade08475 Novel pro	Abb50291 Collagen	Abb90747 Human Tum	Abu54454 Human tum	Abr47418 Breast ca	Abg15191 Novel hum	Ade09399 Novel pro	Abr42661 Decorin-m	Aae02537 Porcine a	0	Aay68425 Type III	Aay68436 Type III
SUMMARIES		OI.	AAB61741	AAB61743	AAE38632	AAR92068	AAE38640	AAY07375	ABU70813	AAU23675	ABG60248	ABG61719	ABU70735	AAW12843	AAW12842	ADE08475	ABB50291	ABB90747	ABU54454	ABR47418	ABG15191	ADE09399	ABR42661	AAE02537	AAB61740	AAY68425	AAY68436
		DB :	4	4	7	~	7	~	9	4	4	Ŋ	9	~	~	7	4	2	9	9	4	7	9	4	4	m	m
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Aay82167 Type II a Aab61742 Human typ		Aar/1/04 Collagen Aay96125 Collagen			Abb09628 Amino aci	Abu19644 Protein e	Aae02534 Bovine al	Aae02533 Bovine al	Aao00933 Human pol	Abp33968 Human ORF	Aag40971 Zea mays	Aay29125 Amino aci	Abm70142 Photorhab	Aaw27523 Murine in	Adb81619 Human ova	Aao03625 Human pol	Aay20721 Human neu
AAY82167 AAB61742	AAB51275	AAX 96125	AAE16478	ABB80736	ABB09628	ABU19644	AAE02534	AAE02533	AA000933	ABP33968	AAG40971	AAY29125	ABM70142	AAW27523	ADB81619	AA003625	AAY20721
11 3 11 4	11 4	1078 3	078 5	078 5	078 5	691 6	1466 4	466 4	133 4	51 5	142 3	674 2	481 6	10 2	57 7	83 4	128 2
87.5			87.5 1						83.3	79.2	79.2	79.2	77.1	72.9	72.9	72.9	72.9
4 4 2 4	4.4	4 4	42	42	42	41	41	41	40	38	38	38	37	32	32	35	35
26 27	238	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

AAB61741 standard; peptide; 9 AA. 20-APR-2001 (first entry) AAB61741; RESULT 1 AAB61741

Human type III collagen carboxy-telopeptide fragment.

Type II collagen; immunoassay; cartilage; telopeptide; human; type III collagen.

Synthetic.

Homo sapiens.

WO200079284-A1.

10-DEC-1999; 28-DEC-2000.

99US-00335098. 99US-0141574P. 99US-0142274P. 99US-0142675P. 99WO-US029357. 29-JUN-1999; 02-JUL-1999; 07-JUL-1999; 17-JUN-1999; 

(WASH-) WASHINGTON RES FOUND.

30-AUG-1999;

Eyre DR;

WPI; 2001-146859/15.

Assay for detecting cross-linked telopeptide analytes indicative of type II collagen resorption in vivo in a body fluid sample, comprises contacting the sample with an antibody which binds to the analyte.

Disclosure; Page 15; 34pp; English.

The invention relates to immunoassays for measuring type II collagen (cartilage) resorption in vivo. The method of analysing a body fluid sample for the presence of an analyte indicative of a physiclogical condition, involves contacting the body fluid sample with an antibody (Ab) which binds to the analyte, detecting binding of Ab in the body fluid sample, and correlating any detected binding to the physiclogical condition. The analysis is useful for measuring type II collagen (cartilage) resorption in vivo, for distinguishing between resorption of

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Mismatches

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assay for detecting cross-linked telopeptide analytes indicative of type II collagen resorption in vivo in a body fluid sample, comprises contacting the sample with an antibody which binds to the analyte.
non-mineralized and mineralized cartilage, and for measuring total cartilage resorption in vivo. The present sequence represents a linear synthetic peptide based on the carboxy-terminal telopeptide sequence of human collagen type III
                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                II collagen; immunoassay; cartilage; telopeptide; human; III collagen.
                                                                             Length 9;
                                                                                                 Indels
                                                                                                                                                                                                                                                             Human type III collagen carboxy-telopeptide fragment.
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                                                                             100.0%; Score 48; DB 4; L 100.0%; Pred. No. 1.4e+06;
                                                                                                  0; Mismatches
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                                                                                                                                                                                                AAB61743 standard; peptide; 12 AA.
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99US-0141574P.
99US-0142274P.
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                                                                                                                                                                                                                                         (first entry)
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                                                          Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                 Synthetic.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                         10-DEC-1999;
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The invention relates to a method of determining the rate of biosynthesis or breakdown of at least one inaccessible biological molecule in a subject. The method is useful for diagnosis or monitoring and treatment of diseases associated with an altered rate of biosynthesis/breakdown of an isotopically labelled precursor molecule, specifically osteoporosis; left-ventricular hypertrophy; liver cirrhosis or fibrosis; congestive heart failure; scleroderma; coal-miner's pneumoconiosis; cardiac or lung fibrosis; Alzheimer's disease; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; muscle-wasting syndromes; muscular dystrophy; athletic training and cancer. The method is also useful for screening candidate gene or protein targets, phenotypic/human validation studies on potential drugs, drug mechanism studies and determining the risk of developing the disease. The present sequence is human C-terminal telopeptide alpha 1. This sequence is used to illustrate the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; therapy; osteoporosis; left-ventricular hypertrophy; scleroderma; liver cirrhosis; congestive heart failure; multiple sclerosis; fibrosis; coal-miner's pneumoconiosis; muscle-wasting syndrome; diabetes mellitus; rheumatoid arthritis; Alzheimer's disease; muscular dystrophy; cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human C-terminal telopeptide alpha 1 #4.
                                                                                                                                                                                                                                                    AAE38632 standard; peptide; 25 AA.
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RESULT 4

Length 12;

DB 4;

Score 48; DB 4 Pred. No. 0.11;

100.0%;

Query Match Best Local Similarity

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Alphal(III)collagen; human; pro-collagen; pro-peptide; artificial skin; proteolytic cleavage site; tissue; biocompatible material; cell culture; suture; haemostatic sponge; tissue augmentation.
                                                                                                                                                note= "any amino acid except Asp'
                                                                                                                                                                   /note= "any amino acid except Glu"
                                                                                                                                                                                                                                                                                                 'note= "any amino acid except Asn"
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                                                     Recombinant alpha1(III)collagen C-terminus.
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AAR92068 standard; peptide; 30
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                                                                                                            Homo sapiens
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                                    27-SEP-1996
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Met."

Recombinant production of collagen - by expressing a pro-peptide-collagen sequence and cleaving at an intermediate proteolytic recognition site. recombinant human collagen polypeptides of the invention. This sequence represents the C-terminal peptide of a recombinant human alphal(III) collagen of the invention. The recombinant pro-collagen of the invention comprises a natural collagen polypeptide chain, a pro-peptide, and a non-natural site-specific proteolypic agent recognition site between the collagen and pro-peptide. The recombinant pro-collagens are used to produce collagens which can be used in tissue and cell cultures. AAR92061-R92069 represent N-terminal and C-terminal peptides of the Recombinant production of collagen

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The collagens can also be used as biocompatible materials such as artificial skin, sutures, haemostatic sponges or tissue augmentation compositions for use in humans. The pro-peptide increases the yield of secreted pro-collagen from cells expressing the recombinant pro-collagen. The increase in yield of the pro-collagen, as compared to cells expressing the collagen chains alone, is at least 1000%
                                                                                                                                                                                                                           Human collagen type I cross-linked C-terminal peptide, PIIICP(alphal).
                                                                                                Gaps
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                                                                            100.0%; Score 48; DB 2; Length 30; 100.0%; Pred. No. 0.28; ive 0; Mismatches 0; Indels
                                                                                                                                                                         AAE38640 standard; protein; 262 AA.
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Best Local Similarity
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                                                           Sequence 30 AA;
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Human, therapy, osteoporosis, left-ventricular hypertrophy, scleroderma, liver cirrhosis; congestive heart failure, multiple sclerosis; fibrosis; coal-miner's pneumoconiosis, muscle-wasting syndrome, diabetes mellitus, rheumatoid arthritis; Alzheimer's disease; muscular dystrophy; cancer; collagen type I cross-linked carboxy-terminal peptide.

WO2003068919-A2

Asp"

Met."

21-AUG-2003

12-FEB-2003; 2003WO-US004183.

12-FEB-2002; 2002US-0356008P.

(REGC ) UNIV CALIFORNIA

Hellerstein MK;

WPI; 2003-689661/65.

Determining rate of biosynthesis or breakdown of inaccessible biological molecules, useful e.g. for diagnosis or monitoring treatment, by administering labeled precursor.

Claim 24; Page 102-103; 105pp; English.

The invention relates to a method of determining the rate of biosynthesis or breakdown of at least one inaccessible biological molecule in a subject. The method is useful for diagnosis or monitoring and treatment of diascases associated with an altered rate, of biosynthesis/breakdown of an isotopically labelled precursor molecule, specifically osteoporosis; left-ventricular hypertrophy; liver cirrhosis or fibrosis; congestive heart failure; scleroderma; coal-miner's pneumoconiosis; congestive heart failure; scleroderma; coal-miner's pneumoconiosis; congestive tibrosis; Alzheimer's disease; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; muscle-wasting syndromes; muscular dystrophy; athletic training and cancer. The method is also useful for screening candidate gene or protein targets, phenotypic/human validation studies on potential drugs, drug mechanism studies and determining the risk of developing the disease. The present sequence is human collagen type I cross-linked carboxy terminal peptide (ICTP). This sequence is used to illustrate the of the invention

Sequence 262 AA;

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Gaps

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Indels

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Mismatches

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9; Conservative

Matches

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colleges such as alcoholic cirrhosis, biliary cirrhosis, hepatitis, schistosomiasis, cardiac fibrosis, Crohn's disease, diabetic nephropathy and fibroses caused by surgery result from an inappropriate nephropathy collagen fibrils. Collagen III is synthesised as a preproprotein which is modified by post-translation modification. The mature collagen III fibrils are generated by cleavage of a propeptide from the C-terminus followed by cleavage of a propeptide from the C-terminus followed by cleavage of a propeptide from the C-terminus followed by cleavage of a propeptide from the C-terminus followed by cleavage of a propeptide from the C-terminus followed by cleavage of a fragment from the N-terminus propeptide [PIIICP]. As the corresponds to the procollagen III C-terminal propeptide [PIIICP]. As the surrounding tissue fluids. The invention relates to an immunoassay to determine PIIICP concentrations and thus diagnose the above diseases and others which result from inappropriate collagen deposition. Different immunoassay may also be used to determine which disease a particular measure the rate of collagen synthesis in patients being treated with glucocorticosteroids in addition the new antibodies may be used in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New immunoassay for procollagen-III-C-terminal propeptide (PIIICP) useful for diagnosing diseases such as alcoholic cirrhosis, hepatitis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alcoholic cirrhosis, biliary cirrhosis; hepatitis; schistosomiasis; cardiac fibrosis; Crohn's disease; diabetic nephropathy; collagen; fibril; procollagen-III-C-terminal propeptide; immunoassay; diagnosis;
                                                                                                 Gaps
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                               DB 7; Length 262;
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Pred. No. 2.7;
                                  100.0%; Score 48; DB
100.0%; Pred. No. 2.6
iive 0; Mismatches
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JUL-1999
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The invention relates to a complex between two interacting proteins in adipocyte cells, given in the specification. The proteins are identified by selecting a bair protein from a known adipocyte marker and then performing a yeast 2-hybrid selection to isolate prey proteins encoded by complex of an adipocyte coNA library. The proteins are designated SID (RTM) (selected interacting domains) proteins. Also included are a polymenteotide encoding a polypeptide in the adipocyte cells, a crocombinant host cell expressing at least one of the interacting copyment to sequences given in the specification (including its fragment or variant), comprising the vector a SID (RTM) polymucleotide comprising any of the 738 mucleotide sequences given in the specification (including its fragment or variant), a SID (RTM) polymucleotide comprising the polympeptides and a comprising the vector, a protein chip comprising the polympeptides and compounds are useful for preventing or treating metabolic disorders such as obesity or diabetes. The polymucleotides are useful as probes or primers. The complex is preventing or treating metabolic disorders such as obesity or diabetes. The polymucleotides are useful as probes or primers. The complex is complex preventing drugs that modulate the protein interacting domains sld control of particularly useful for identifying selected interacting domains (STM) (RTM)) for screening drugs that modulate the protein interaction, thus exhibiting the therapeutic effect. The present sequence represents a SID (CTM) protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wew complex between two interacting proteins in adipocyte cells, useful for identifying selected interacting domains that modulate protein interactions, or for preventing or treating metabolic disorders such as obesity or diabetes.
                                                                                                                                                                                                                                                                                        Human; prey; adipocyte; SID; selected interacting domain; anorectic; antidiabetic; protein-protein interaction; diabetes; yeast 2-hybrid assay; metabolic disorder; obesity.
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                                                                                                                                                                                                                                                  Human adipocyte Selected Interacting domain, SID, #444.
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Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6; Page 258-259; 382pp; English.
                                                                                                                                      ABU70813 standard; protein; 293 AA.
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                                                                                                                                                                                                                   (first entry)
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N-PSDB; ACA57357.
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Best Local Similarity
                                       12 IGGEKAGGF
1 IGGEKAGGF
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                                                                                                                                                                                                                                                                                                                                                                                                                    WO200286122-A2
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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2000US-0231243P
2000US-0231244P
2000US-0231413P
2000US-0232800P
2000US-0232080P
2000US-0232081P
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2000US-023423P.
2000US-0234274P.
2000US-0234997P.
2000US-023598P.
2000US-0235834P.
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2000US-0236370P.
2000US-0236802P.
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2000US-0244617P.
2000US-0246474P.
2000US-0246476P.
2000US-0246476P.
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2000US-0246528P.
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2000US-0246609P.
          2000US-0230437P.
2000US-0230438P.
2000US-0231242P.
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2000US-0241808P
2000US-0241809P
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2000US-0239935P
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2000US-0241785P
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2000US-0246525P
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                 06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
                                                           08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
12-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
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08-NOV-2000;
08-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
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17-NOV-2000;
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                                                                                                                                             Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; reproductive disorder; nephrotropic; anticagulant,
 Gaps
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  Indels
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Mismatches
                                                                                                                             Novel human enzyme polypeptide #761
                                                                           AAU23675 standard; protein; 309 AA
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                                                                                                                                                                                                                                                                           2000US-0179065P.
2000US-0180628P.
2000US-018464P.
2000US-0189874P.
2000US-0190076P.
2000US-01913P.
2000US-020551SP.
2000US-020551SP.
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2000US-0217487P.
2000US-0217496P.
2000US-0218290P.
2000US-0220963P.
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2000US-0225267P.
2000US-0225268P.
2000US-0225270P.
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2000US-0215135P.
2000US-0216647P.
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2000US-0225213P.
2000US-0225214P.
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2000US-0229345P
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                                                                                                            (first entry)
9; Conservative
                                 139 IGGEKAGGF 147
                 1 IGGEKAGGF 9
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26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
22-AUG-2000;
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18-APR-2000;
19-MAY-2000;
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28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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01-SEP-2000;
05-SEP-2000;
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                                                                                            AAU23675;
Matches
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Human ovarian antigen #10.

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The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of diagnosis, treatment, prevention and/or prognosis of a wide range of immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. AIDS) autoimmune disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polymucleotides of the invention can also be used in gene therapy. AAU22915-AAU23814 represent the novel human enzyme polypeptides of the invention. Note: The sequence the novel human enzyme polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but were sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polypeptides and polymucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barash SC, Ruben SM;
               17-NOV-2000; 2000US-0249218P.

17-NOV-2000; 2000US-0249244P.

17-NOV-2000; 2000US-0249264F.

17-NOV-2000; 2000US-0249264F.

17-NOV-2000; 2000US-0249265P.

17-NOV-2000; 2000US-024920P.

17-NOV-2000; 2000US-0249300P.

01-DEC-2000; 2000US-0249300P.
                                                                                                                                                                                                                      05-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-0251988P.
05-DEC-2000; 2000US-02561719P.
06-DEC-2000; 2000US-0251479P.
08-DEC-2000; 2000US-0251468P.
08-DEC-2000; 2000US-0251868P.
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2000US-0251990P
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08-DEC-2000;
11-DEC-2000;
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                                                                                                             100.0%; Score 48; DB 4; Length 309; 100.0%; Pred. No. 3.1; 0; Mismatches 0; Indels
                                                                                                                                   ABG60248 standard; protein; 309 AA.
                                                                                                                  9; Conservative
                                                                                                                         51 IGGEKAGGF 59
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Query Match Best Local Similarity

Matches

1 IGGEKAGGF

13-AUG-2002 (first entry)

ABG60248;

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RESULT 9 ABG60248

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Human; ovarian antigen; ovary disorder; breast disorder; neoplastic disorder; cancer; infectious disease; inflammatory disease; preproductive system disorder; autoimmune disorder; Alzheimer's disease; blood-related disorder; hyperproliferative disorder; hair loss; urinary system disorder; hyperproliferative disorder; hair loss; respiratory disorder; cardiovascular disorder; arrhythmia; respiratory disorder; musculoskeletal system disorder; and meural activity disorder; neurological disorder; endocrine disorder; gastrointestinal disorder; luver disorder; pancreatic disorder; disorder; inherited disorder; large intestine disorder; developmental disorder; inherited disorder; wound healing; skin aging; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-SEP-2000; 2000US-0232398P.
17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-0250166P.
08-DEC-2000; 2000US-0251868P.
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2000US-0209467P
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                                                                                                                                                                                                                                                                                                                                                                    preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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07-JUN-2000;
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Novel isolated human ovarian related polypeptide useful for diagnosis/treatment of disorders of ovary and breast such as neoplastic disorders, infectious diseases, inflammatory diseases, and reproductive disorders

Claim 11; SEQ ID NO 78; 524pp; English.

The invention relates to isolated ovarian related polypeptide (ovarian antigen) comprising a sequence at least 90% identical to a sequence selected from a polypeptide fragment, domain, epitope or full length protein of a sequence (S1) appearing as ABG6029-ABG60296 having protein of a sequence (S1) appearing as ABG60239-ABG60296 having conflored activity, or a variant, allelic variant or species homologue of S1. Also included are the CDNA clones encoding the proteins of S1. S1, an anti-S1 antibody and the CDNA clones encoding the proteins of S1. S1, conformed anti-S1 antibody and the CDNA are useful for diagnosing, preventing, treating or ameliorating a medical condition in mammalian subject complastic disorders (such as ovarian Krukenberg tumour and cancer). Infectious diseases (e.g., mastitis), inflammatory disorders (systemic lupus erythemberg tumour and cancer).

C1 (e.g., abscesses), reproductive system disorders (page of disease), autoimmune disorders (systemic lupus erythematosus, rheumatoid arthritis), blood-related disorders (sickle cell anaemia).

C2 autoimmune disorders (systemic lupus erythematosus, rheumatoid arthritis), blood-related disorders (sickle cell anaemia).

C3 arthritis), blood-related disorders (sickle cell anaemia), respiratory disorders (latenders, neural activity and disorders (latenders) disorders (latenders) (inflammatory disorders), liver disorders, disorders of the large intestine, cendocrine disorders (Asorders, disorders of the large intestine, developmental and inherited disorders, disorders of the large intestine, cendocrine disorders, disorders disorders of the large intestine, cendocrine disorders, disorders, disorders of the large intestine, cendocrine disorders (disorders, disorders of the large intestine, cendocrine disorders), liver disorders, disorders of the large intestine, cendocrine disorders (disorders, disorders of the large intestine, cendocrine disorders, disorders, disorders disorders, disorders disorders, disorders, disorders disorders disorders, disorders dis

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Ovarian related polypeptide; neoplastic disorder; tumour; ovarian cancer; hyperproliferative disorder; adult acute lymphocytic leukaemia; breast cancer; reproductive system disorder; tuberculosis; arthritis; immune system disorder; Chediak-Higashi's syndrome; neonatal neutropenia; autoimmune disorder; Hashimoto's thyroiditis; inflammatory disorder; septic shock; multiple sclerosis; central nervous system disorder; neutrological disorder; allergy; Parkinson's disease; Alzheimer's disease; cardiovascular disorder; atherosclerosis; blood related disorder; respiratory disorder; urinary system disorder; musculoskeletal disorder; osteoporosis; wound healing; endocrine disorder; infectious disease; gastrointestinal disorder; transplantation; food additive; preservative.
as food additive or preservative. The present sequence represents an ovarian antigen, SI protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published.pot sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                        Gaps
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0
                                                                                                                 100.0%; Score 48; DB 4; Length 309; 100.0%; Pred. No. 3.1; cive 0; Mismatches 0; Indels
                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                            Novel ovarian related polypeptide #10
                                                                                                                                                                                                                               ABG61719 standard; protein; 309 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0217496P.
2000US-0218290P.
2000US-0220963P.
2000US-0220964P.
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2000US-0209467P.
2000US-0214886P.
2000US-0215135P.
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2000US-0216880P.
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2000US-0184664P.
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2000US-0190076P.
2000US-0198123P.
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2000US-0225266P
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                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                     9; Conservative
                                                                                                                                                                        51 IGGEKAGGF 59
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                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                         1 IGGEKAGGF
                                                                                               Sequence 309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2002045230-A1
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14-JUL-2000; 2
26-JUL-2000; 2
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24-FBB-2000;
02-MAR-2000;
11-MAR-2000;
11-MAR-2000;
11-MAY-2000;
19-MAY-2000;
29-JUN-2000;
28-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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2000US-02257579-
2000US-0225758P-
2000US-0226279P-
2000US-0226681P-
2000US-0226681P-
2000US-0226868P-
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2000US-0228924P.
2000US-029343P.
2000US-0229344P.
2000US-0229344P.
2000US-0229344P.
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2000US-0232397P.
2000US-0232398P.
2000US-0232399P.
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2000US-0232401P.
2000US-0233063P.
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2000US-0235834P.
2000US-0235836P.
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2000US-0234274P.
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14-AUG-2000;
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30-AUG-2000;
01-SEP-2000;
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05-SEP-2000;
06-SEP-2000;
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01-NOV-2000;
08-NOV-2000;
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22-AUG-2000;
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(RUBI/) RUBIN S M. (BARA/) BARASH S C.

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08-NOV-2000; 2000US-0246526P.
08-NOV-2000; 2000US-0246537P.
08-NOV-2000; 2000US-0246532P.
08-NOV-2000; 2000US-0246532P.
08-NOV-2000; 2000US-0246610P.
08-NOV-2000; 2000US-0246610P.
08-NOV-2000; 2000US-0246611P.
08-NOV-2000; 2000US-0246611P.
17-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249218P.
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17-NOV-2000; 2000US-0249218P.
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17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249244P.
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17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-0259391P.
05-DEC-2000; 2000US-0251931P.
05-DEC-2000; 2000US-025193P.
06-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-025186P.
08-DEC-2000; 2000US-025186P.
08-DEC-2000; 2000US-025186P.
08-DEC-2000; 2000US-025198P.
08-DEC-2000; 2000US-025198P.
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11-DEC-2000; 200US-025198P.
11-DEC-2000; 200US-025198P.
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2001US-00764888.
2001US-00764891.
2001US-00764892.
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17-JAN-2001; 2001US-00764870.
17-JAN-2001; 2001US-00764874.
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2001US-00764898.
2001US-00764902.
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(ROSE/) ROSEN C A.

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New complex between two interacting proteins in adipocyte cells, useful for identifying selected interacting domains that modulate protein interactions, or for preventing or treating metabolic disorders such as
                  Gaps
                                                                                                                                          Human; prey; adipocyte; SID; selected interacting domain; anorectic; antidiabetic; protein-protein interaction; diabetes; yeast 2-hybrid assay; metabolic disorder; obesity.
                  .
0
   100.0%; Score 48; DB 5; Length 309; 100.0%; Pred. No. 3.1;
                   Indels
                                                                                                                             Human adipocyte Selected Interacting domain, SID, #366.
                   .
                   0; Mismatches
                                                                                    ABU70735 standard; protein; 339 AA
                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 229; 382pp; English.
                                                                                                                                                                                                                     14-MAR-2002; 2002WO-EP003768
                                                                                                                                                                                                                                   14-MAR-2001; 2001US-0275734P
                                                                                                                  10-JUN-2003 (first entry)
51 IGGEKAGGF 59
                                                                                                                                                                                                                                                                Legrain P, Daviet L;
                                                                                                                                                                                                                                                                               WPI; 2003-103412/09.
N-PSDB; ACA57279.
                                  1 IGGEKAGGF 9
                                                                                                                                                                                                                                                   (HYBR-) HYBRIGENICS.
                                                                                                                                                                                                                                                                                                                           obesity or diabetes
                                                                                                                                                                                          WO200286122-A2
                                                                                                                                                                            Homo sapiens.
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                                                                                                   ABU70735;
                                                                       RESULT 11
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Gaps

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This sequence represents a chimeric procollagen molecule of the invention. This sequence has the procollagen C-prepropeptide from the pro-alphal (III) chain sequence. The C-propeptide is implicated in the assembly of the monomer chains into trimerised pro-alpha chains prior to cleavage of the N- and C-propeptides and formation of Collagen in fibril-forming pro-alpha chains. The C-propeptides determine the type-specific assembly of the moieties to which they are attached. The molecule of the invention comprises a first moiety, which is an alien collagen alpha-chain or a non-collagen material. The convel collagen molecule can be used for treatment or diagnosis in humans or animals, especially for the treatment of procollagen material. The covalings with reduced scarring or for use in photography, brewing diseases with reduced scarring or for use in photography, brewing containing substitutions in the recognition site, may have significantly when the containing substitutions in the recognition site, may have significantly convent containing substitutions in the recognition site, may have significantly convents.
                                                                                                                                                                                                                                                                                                                                                                                                    C-propeptide, recognition sequence; procollagen; monomer chain; therapy; trimerised pro-alpha chain; fibril; procollagen suicide; wound healing; fibrotic disease; human; chimeric protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel pro:collagen mol. - comprising pro:collagen C-pro:peptide attached to an alien collagen alpha-chain or non-collagen material, useful e.g.
                                                                    100.0%; Score 48; DB 6; Length 339; 100.0%; Pred. No. 3.4; or Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                     Pro-alphal(III):(I) CP chimeric protein.
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                                                                                                                                                                                                                                                             AAW12843 standard; peptide; 623 AA.
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 (prey) protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95GB-00017773.
96GB-00006152.
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                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                       Conservative
                                                                                                                                                                         81 IGGEKAGGF 89
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                                               Query Match
Best Local Similarity
''... 9; Conserv?
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                                                                                                                                        1 IGGEKAGGF
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                                  Sequence 339 AA;
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23-MAR-1996;
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This sequence represents a truncated procollagen pro-alphal(III) chain that can be used in the procollagen molecules of the invention. The C-propeptide is implicated in the assembly of the monomer chains into trimerised pro-alpha chains prior to cleavage of the Monomer Chains into crimerised pro-alpha chains prior to cleavage of the N- and C-propeptides and formation of collagen in fibril-forming pro-alpha chains. The C-collagen cattached, The molecule of the invention comprises a first moiety having procallagen C-propeptide activity attached to a second moiety, which is an alien collagen alpha-chain or a non-collagen material. The novel collagen molecule can be used for treatment or diagnosis in humans or animals, especially for the treatment of procollagen suicide, as an adhesive or implant, to promote (chronic) wound healing or fibrotic diseases with reduced scarring or for use in photography, brewing, containing substitutions in the recognition site, may have significantly altered properties and characteristics, such as different binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel pro:collagen mol. - comprising pro:collagen C-pro:peptide attached to an alien collagen alpha-chain or non-collagen material, useful e.g.
                                                                                                                                                                                                                                                                                                  C-propeptide; recognition sequence; procollagen; monomer chain; therapy; timerised pro-alpha chain; fibril; procollagen suicide; wound healing;
                      Gaps
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100.0%; Pred. No. 6.4;
ive 0; Mismatches 0; Indels
                    Indels
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   Pred. No. 6.4; Mismatches
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                                                                                                                                                                AAW12842 standard; protein; 626 AA.
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                                                                                                                                                                                                                                                                   Truncated pro-alphal (III) chain.
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 100.0%;
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                   Conservative
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                   fibrotic disease; human.
                                                                                 368 iddekadde 376
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                                                  1 IGGEKAGGF
Best Local Similarity
Matches 9, Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for wound healing
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14-JUN-1996;
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                                                                                                                                                                                                 AAW12842;
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                                                                                                                                   RESULT 13
                                                                                                                                                   AAW12842
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Ovarian tumour marker gene; human; overexpression; upregulation; epithelial tumour; cancer; diagnosis; prognosis; disease monitoring; identification; serous cystadenoma; borderline serous tumour; serous cystadenoma; mucinous cystadenocarcinoma; mucinous cystadenoma; mucinous cystadenoma; mudifferentiated carcinoma; clear cell adenocarcinoma; cystadenomi, adenofibroma; adenofibroma; serial analysis of gene expression; SAGE; immune response pathway; cell proliferation regulation; protein folding; membrane localised; secreted; therapeutic target; cytostatic;

gene therapy; vaccine

WO200175177-A2 sapiens.

Ното

11-OCT-2001.

Collagen type III alpha-1 ovarian tumour marker protein, SEQ ID NO:72.

(first entry)

08-FEB-2002

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New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang J;
Wang Z;
                                                                                                                                                                                                                                                                                                                                                                                                          novel gene; novel protein; tissue marker; molecular weight marker; chromosome marker; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang J, Zhao QA,
ou P, Drmanac RT,
                                                                                                                                                                                                                                                                                                                                            Novel protein (useful for identifying genetic disorders) #630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 7; Length 842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goodrich RW, Ren F, Zhang
ehrman T, Weng G, Zhou P,
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100.0%; Pred. No. 8.7
:ive 0; Mismatches
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Ghosh M, Xue AJ, Wehrman T, Weng G, Zh
Ma Y. Wang D, Chen R, Xu C, Boyle BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; SEQ ID NO 1541; 1177pp; English
                                                                                                                                                               ADE08475 standard; protein; 842 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002US-03723B1P.
2002US-0372615P.
2002US-00128558.
2002US-0376045P.
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2002US-0365091P.
2002US-0365384P.
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                                                                                                                                                                                                                                                                                     (first entry)
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   368 IGGEKAGGF 376
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14-MAR-2002;
14-MAR-2002;
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Detecting and identifying ovarian tumor, identifying increased risk for developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor marker

Claim 23; Page 114-117; 140pp; English.

Pizer ES, Hough CD;

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

03-APR-2001; 2001WO-US010947 03-APR-2000; 2000US-0194336P Sherman-Baust CA,

Morin PJ,

WPI; 2001-626450/72.

N-PSDB; ABA83117

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The invention relates to methods for diagnosing and prognosing ovarian tumours in an individual via the detection and measurement of the tumours in an individual via the detection and measurement of the tumours in an individual via the detection and measurement of the expression of ovarian tumour in a patient, for identifying an individual at increased risk for developing ovarian cancer, in prognostic tests for assessing the relative seveloping ovarian cancer, in tests for assessing the relative seveloping ovarian cancer, in tests for monitoring a patient in remission from ovarian cancer. The methods can additionally be used to identify a particular tumour as monitoring disease status in a patient being treated for ovarian cancer. The methods can additionally be used to identify a particular tumour as being an ovarian tumour (i.e., an epithelial ovarian tumour selected from serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma, contained and procarcinoma, endometricid carcinoma, undelferentiated carcinoma, clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner cumour. The ovarian tumour marker genes of the invention were found to be overexpressed in a broad variety of ovarian epithelial tumour cells crelative to normal ovarian pathways, in the regulation of cell confideration and in protein folding, and many of these are membrane confect and an expense for their each encoded confideration and may be overed for their use as diagnostic and encoded confideration and the ovarian tumour marker genes or their encoded confideration and the povarian epithelial relative to secreted. In addition to their use as diagnostic and confideration and the ovarian tumour marker genes or their encoded confideration and the povarian tumour marker genes or their encoded confideration and the provered for their expense.
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ABB50291 standard; protein; 1466 AA.

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Search completed: September 18, 2004, 04:25:32 Job time : 49.1765 secs

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Sequence 20, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 40, Appl
Sequence 42, Appl
Patent No. 5473052
Sequence 21, Appl
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27825, A
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Sequence 43, App
                                                                                                                                                      September 18, 2004, 04:20:54; Search time 14.8235 Seconds (without alignments) 31.344 Million cell updates/sec
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Compugen Ltd.
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US-09-500-811-21
US-09-548-608-21
US-09-252-991A-26476
US-09-252-991A-26608
US-08-252-991A-26608
US-08-702-110A-19
US-08-702-110A-19
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GenCore version
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                        Run on:
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Segmenter 20078														, L	Segmence 15. Appl	Segmence 15. April	Sequence 90, Appl
US-09-252-991A-20078	US-09-252-991A-28522	US-09-252-991A-27659	US-09-252-991A-23300	US-09-252-991A-22479	US-09-621-976-6612	US-09-252-991A-28805	US-09-252-991A-30541	US-09-252-991A-22621	US-08-602-359A-41	US-09-252-991A-30116	US-09-489-039A-13982	US-10-009-999A-39	US-08-963-825-15	US-09-500-811-15	US-09-570-573-15	US-09-548-608-15	US-08-383-753-90
4	4	4	4	4	4	4	4	4	~	4	4	4	m	4	4	4	н
168	284	529	540	822	70	221	227	254	311	551	942	9	7	7	7	7	15
70.8	70.8	70.8	70.8	70.8	68.8	68.8	68.8	68.8	68.8	68.89	68.8	66.7	66.7	66.7	66.7	66.7	66.7
34	34	34	34	34	33	33	33	33	33	33	33	32	32	32	32	32	32
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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FARENT NO. SOLUZANO.

FARENT INPORMATION:

APPLICANT: Eyre, David R.

TITLE OF INPORMATION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS

FILE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS

FILE OF INVENTION NUMBER: US/10/009,999A

CURRENT FILING DATE: 2003-01-22

PRIOR PELING DATE: 1999-12-10

PRIOR APPLICATION NUMBER: US 09/335,098

PRIOR PLING DATE: 1999-12-10

PRIOR PLING DATE: 1999-06-17

PRIOR PLING DATE: 1999-06-29

PRIOR PLING DATE: 1999-06-29

PRIOR PLING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-07

PRIOR PLING DATE: 1999-08-30

PRIOR FILING DATE: 1999-08-30

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PATENTIN VERSION 3.2

SEQ ID NO 41

LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: synthetic peptide corresponding to carboxy-terminal; OTHER INFORMATION: telopeptide sequence of human type III collagen US-10-009-999A-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Patent No. 6602980
GENERAL INFORMATION:
APPLICANT: Eyre, David R.
TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                          Sequence 41, Application US/10009999A Patent No. 6602980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 9; Conservative
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-10-009-999A-41
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                                                                                                                                                                                         ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 48; DB 3; Length 626;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 48; DB 3; Length 623; 100.0%; Pred. No. 1.8;
                                                                                                                                     Query Match 100.0%; Score 48; DB 4; Length 15; Best Local Similarity 100.0%; Pred. No. 0.047; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRNERAL INFORMATION:
APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER; TITLE OF INVENTION: NOVEL PROCOLLAGENS
FILE REFERENCE: 408769579US LISTING
CURRENT APPLICATION NUMBER: US/09/029,348
CURRENT FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MANCHESTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         Gequence 3, Application US/09029348; Patent No. 6171827; GENERAL INFORMATION: APPLICANT: TITLE OF INVENTION: NOVEL PROCOLLAGENS; FILE REFERENCE: 4087857PUS LISTING; CURRENT APPLICATION NUMBER: US/09/029,348; CURRENT FILING DATE: 1998-05-07; NUMBER OF SEQ ID NOS: 20; SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-029-348-2; Sequence 2, Application US/09029348; Patent No. 6171827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 9; Conservative
                  STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 IGGEKAGGF 376
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TYPE: amino acid
                                                                                            US-08-278-774-20
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LENGTH: 623
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US-09-029-348-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MISC FEATURE OTHER INFORMATION: synthetic peptide corresponding to carboxy-terminal OTHER INFORMATION: telopeptide sequence of human type III collagen
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Sequence 20, Application US/08278774

Patent No. 6653450

GENERAL INPORMATION:
APPLICANT: Barg, Richard A
APPLICANT: Toman, David P
APPLICANT: Toman, David P
APPLICANT: Wallace, Donald
TITLE OF INVENTION: MUTATED RECOMBINANT COLLAGENS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: COLLAGEN CORPORATION
STREET: 2500 Faber Place
CITY: Palo Alto
CITY: QALLO ALTO
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,774
FILING DATE: 22-Jul-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rafayko, Kathi L
REGISTRATION NUMBER: 34,644
REFERENCE/DOCKET NUMBER: 34,644
REFERENCE/DOCKET NUMBER: 94.018
TELECOMMUNICATION INFORMATION:
                       CURRENT APPLICATION NUMBER: US/10/009,999A
CURRENT PILING DATE: 2003-01-22
PRIOR PELING DATE: 1999-12-10
PRIOR PLING DATE: 1999-12-10
PRIOR PILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: US 09/335,098
PRIOR PILING DATE: 1999-06-17
PRIOR PILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-07-02
PRIOR PILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: US 60/142,675
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/142,675
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 09/385,740
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 45
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TELEFAX: (415) 354-4752
TELEX:
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SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 iGGEKAGGF 12
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Best Local Similarity
Matches 9; Conserv
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FILING DATE:
CLASSIFICATION: 436
                                                                               ; US-10-009-999A-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-963-825-21
FEATURE:
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                                                                               Fedence 40, Application US/10009999A
Fedence 40, Application US/10009999A
Fedence 40, Application US/10009999A
GENERAL INFORMATION:
FAPLICANT: Eyre, David R.
TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS
FILE REFERENCE: WROS-1-1802
CURRENT FILING DATE: 2003-01-22
FRIOR PELIOR DATE: 1999-12-10
FRIOR APPLICATION NUMBER: US 09/335,098
FRIOR FILING DATE: 1999-66-17
FRIOR PELIOR DATE: 1999-66-17
FRIOR FILING DATE: 1999-06-17
FRIOR FILING DATE: 1999-06-29
FRIOR FILING DATE: 1999-06-29
FRIOR FILING DATE: 1999-06-29
FRIOR APPLICATION NUMBER: US 60/142,274
FRIOR APPLICATION NUMBER: US 60/142,675
FRIOR APPLICATION NUMBER: US 60/142,675
FRIOR APPLICATION NUMBER: US 60/142,675
FRIOR APPLICATION NUMBER: US 09/385,740
FRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 45
SEQ ID NOS: 45
SEQ ID NOS: 45
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Fatent No. 6602980
GENERAL INFORMATION:
TITLE OF INVENDATION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS
FILE REFERENCE: WROS-1-18220
CURRENT APPLICATION NUMBER: US/10/009,999A
CURRENT FILING DATE: 2003-01-22
PRIOR FILING DATE: 1999-12-10
PRIOR PELICATION NUMBER: US 09/335,098
PRIOR FILING DATE: 1999-06-19
PRIOR FILING DATE: 1999-06-19
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-03
PRIOR FILING DATE: 1999-07-03
PRIOR FILING DATE: 1999-07-03
PRIOR FILING DATE: 1999-07-03
PRIOR FILING DATE: 1999-07-03
PRIOR FILING DATE: 1999-07-03
PRIOR FILING DATE: 1999-07-03
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ 1D NOS: 45
SOFTWARE: DatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MISC FEATURE
OTHER INFORMATION: synthetic peptide corresponding to carboxy-terminal
OTHER INFORMATION: telopeptide sequence of human type III collagen
US-10-009-999A-40
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100.0%; Pred. No. 38+05;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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1 IGGEKAGG 8
                                                            -10-009-999A-40
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Sequence 21, Application US/08963825

Patent No. 6110689

GENERAL INFORMATION:

APPLICANT: Qvist, Per

APPLICANT: Qvist, Per

APPLICANT: Bonde, Martin

TITLE OF INVENTION: A Method for Assaying Collagen Fragments

TITLE OF INVENTION: A Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of TITLE OF INVENTION: Disorders Associated with the Metabolism of TITLE OF INVENTION: Disorders Associated with the Metabolism of STRESPONDENCE ADDRESS:

ADDRESSEE: Darby & Darby PC

STREET: 805 Third Avenue

STREET: New York

STATE: New York

COUNTRY: USA
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NAME/KEY: MISC FEATURE OTHER INFORMATION: synthetic peptide corresponding to carboxy-terminal OTHER INFORMATION: telopeptide sequence of human type III collagen
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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;PRICENT NO. 5473052
;PRICENT NO. 5473052
;PRICENT NO. 5473052
;TILE OF INVENTION: ANTHGEN BINDING FRAGMENTS OF AN ANTIBODY
;TO TYPE-I COLLAGEN ANINO-TERMINAL TELOPEPTIDE
;TO TYPE-I COLLAGEN ANINO-TERMINAL TELOPEPTIDE
;CURRENT APPLICATION ANTHS: 30
;CURRENT APPLICATION NUMBER: US/08/221,705
;FILING DATE: 01-APR-1994
;FILING DATE: 01-APR-1990
;FILING DATE: 01-DEC-1989
;FILING DATE: 01-DEC-1989
;FILING DATE: 01-DEC-1989
;FILING DATE: 01-DEC-1989
;FILING DATE: 01-DEC-1989
;FILING DATE: 06-NOV-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
                                                                                                                                87.5%; Score 42; DB 4; Length 11; 100.0%; Pred. No. 0.35; ative 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/963,825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.5%; Score 42; DB 6;
88.9%; Pred. No. 0.35;
live 0; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                       Conservative
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                                                                                                                                Query Match
Best Local Similarity
Matches 8; Conserv
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TITLE OF INVENTION:

A Method for Assaying Collagen Fragments
TITLE OF INVENTION:
In Body Fluids, A Feet Kit and Means for Carrying Out the
TITLE OF INVENTION:
MEthod and Use of the Method to Diagnose the Presence of
TITLE OF INVENTION:
Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES:
ADDRESSEE:
ADDRESSEE: Darby & Darby PC
STREET:
805 Third Avenue
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88.9%; Pred. No. 31;
tive 0; Mismatches 1; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/570,573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4305/08701
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APPLICALL...
ATTORNEY/AGENT INFORMATION:
NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 236697
TELERX: 236697
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APPLICATION NUMBER: 08/187,319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-570-573-21
; Sequence 21, Application US/09570573
Patent No. 6342361
; GENERAL INFORMATION:
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IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (III)
                                                                                                                                                                                         IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (III)
                                                                                                                                                                                                                                                                                                              unery Match 87.5%;
Best Local Similarity 88.9%;
Matches 8; Conservative
: 1078 amino acids amino acids
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APPLICANT: Bonde, Martin
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                                                                                                                                                               ORGANISM: Homo sapiens
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                           MOLECULE TYPE: protein ORIGINAL SOURCE:
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Best Local Similarity
                                                                 linear
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
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                                       TYPE: ami
TOPOLOGY:
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Sequence 21. Application US/09500811

Patent NO. 6323314

GENERAL INFORMATION:
APPLICANT: Goviet, Per APPLICANT: Bonde, Martin
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,811
      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/187,319
FILING DATE: 21-JAN-1994
ATTORNEY, AGENT INFORMATION:
NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELECHHONE: 212-527-7700
TELEFAX: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4305/08701
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ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: GOGOTIE, Adda C
REGISTRATION NUMBER: 9,714
REFERENCE/DOCKET NUMBER: 4305
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEPHONE: 212-537-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Darby & Darby PC
805 Third Avenue
                                                                                                                                                                                                                                                                                                                           TELEX: 236687
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                         : 1078 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 236687
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1061 iGAEKAGGF 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-963-825-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1990-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27825, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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Pred. No. 91;
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91;
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                                                                                                   APPLICANT: TSONGAIS, JOHN
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361002
CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
PRIOR PILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SOFTWARE: FARESEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
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Best Local Similarity 75.0%; Pred. No. 91;
Matches 6; Conservative 2; Mismatches
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BER: US 60/074,788
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; Sequence 26476, Application US/09252991A
; Patent No. 6551795
Rahme, Laurence G.
Mahajan-Miklos, Shalina
Tan, Man-Wah
                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 75.0%;
                                                                                       Drenkard, Eliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
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413 VGGDKAGG 420
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US-09-252-991A-27825
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                                                           APPLICANT:
APPLICANT:
APPLICANT:
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                                           APPLICANT
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APPLICANT: Qvist, Per
APPLICANT: Qvist, Per
APPLICANT: Qvist, Per
APPLICANT: Qvist, Per
APPLICANT: Bonde, Martin

TITLE OF INVENTION: A Method for Assaying Collagen Fragments

TITLE OF INVENTION: Body Fluids, A Test Kit and Means for Carrying Out the
TITLE OF INVENTION: Disorders Associated with the Metabolism of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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88.9%; Pred. No. 31;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/548,608
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4305/08701
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                                                                                                                                       US-09-548-608-21
; Sequence 21, Application US/09548608
; Patent No. 6355442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTOMACIA
NAME: GOGORIS, Adda C
REGISTRATION NUMBER: 29,714
REPERENCE/DOCKET NUMBER: 4305
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-57-7700
TELEFAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE: CLONE: COLLAGEN ALPHA 1 (III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 236687
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gogoris, Adda C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 86.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                     1061 IGAEKAGGF 1069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1061 İGAEKAĞĞF 1069
         1 IGGEKAGGF 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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0; Gaps

Search completed: September 18, 2004, 04:32:22 Job time: 15.8235 secs

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Sequence 13, Appl
Sequence 11, Appl
Sequence 19, Appl
Sequence 78, Appl
Sequence 72, Appl
Sequence 72, Appl
Sequence 31, Appl
Sequence 31, Appli
Sequence 31, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 12, Appli
                                                                                                                         September 18, 2004, 04:29:56; Search time 42.7059 Seconds (without alignments) 67.677 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 40,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/REUTS_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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| Cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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| Cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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| Cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-918-715-226
US-10-257-021-72
US-10-10-257-021-72
US-10-31-822-33
US-10-357-851-3
US-10-358-024-3
US-10-734-564-103
US-10-734-564-103
US-10-402-089-12
US-10-402-072A-12
US-10-615-959-40
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US-10-615-959-43
US-10-366-125-11
US-10-366-125-19
US-09-908-711-78
                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                   1342398 seqs, 321133274 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published_Applications_AA:*
                                                                                OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                 US-10-615-959-41
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Match Length DB
                                                                                                                                                                                                                                                         1 IGGEKAGGF 9
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Perfect score:
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•	v -	47	equence 4.	Sequence 6. App	equence	equence	equence	Sequence 5882.	137	Sequence 51, Appl	Sequence 1899		equence 10346	16532	Sequence 24908	19009	55	equence 78		e 19	Sequence 20	Sequence 29	Sequence 27910	Sequence 18950	Sequence 21507	Sequence 15103	Sequence 16702	Sequence 2312	Sequence 10781
0-319-10-515-0	US-10-058-124-2	US-10-282-122A-4756	US-10-402-089-4	US-10-405-	US-10-402-	US-10	US-10-424-	US-09-864-408A-	US-10-437-963-13765	US-09-975-719	US-10-437-963-1	US-10-437-963-10600	US-10-437-963-10	US-10-437-9	US-10-424-599-24908	US-10-424-599-19009	US-10-425-114-5524	US-10-156-761-784	US-09-848-585-1	-10-642-	-10-424-599-2	3-10-029-386-	S-10-424-599-2	-10-437-963-1	-10-424-59	-10-437-963-1	-10-424-599-16702	-10-424-599-2312	7-963-10781
5	14	12	15	15	15	15	12	디	16	10	16	16	16	16	12	12	12	14	6	16	12	14	12	16	12	16	12	12	16
-	1078	691	46	46	1466	1466	53	51	322	674	969	225	488	696	73	155	284	353	10	10	43	46	53	9	63	68	70	96	98
	87.5	85.4	85.4	85.4		85.4	81.2	79.2	79.2	79.2	79.2	77.1	77.1	77.1	75.0				72.9										
4.2	42	41	41	41	41	41	39	38	38	38	38	37	37	37	36	36	36	36	32	35	32	35	32	32	32	32	35	35	35
16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

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RESULT INCRANTION:
US-10-615-959-41
Sequence 41, Application US/10615959
Fublication No. US20040048321A1
GENERAL INFORMATION:
TITLE OF INVENTION: SYMTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS
FILE REFERENCE: WROS-1-18220
CURRENT APPLICATION NUMBER: US/10/615,959
FRIOR APPLICATION NUMBER: US/10/009,99A
PRIOR FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: US 60/141,574
PRIOR FILING DATE: 1999-06-19
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-07-02
PRIOR PELING DATE: 1999-07-02
PRIOR PELING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
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PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE:
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Score 48; DB 12; Length 9; Pred. No. 1.2e+06;

100.0%; 100.0%;

Query Match Best Local Similarity ö

Gaps

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g à

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APPLICANT: Hellerstein, Marc
APPLICANT: Hellerstein, Marc
TITLE OF INVENTION: MESGREMENT OF BIOSYNTHESIS AND BREAKDOWN RATES OF
TITLE OF INVENTION: BIOLOGICAL MOLECULES THAT ARE INACCESSIBLE OR NOT
TITLE OF INVENTION: BASILY ACCESSIBLE TO DIRECT SAMPLING, NON-INVASIVELY,
TITLE OF INVENTION: CATABOLITIC PRODUCTS
FILE REFERENCE: 416272003500
CURRENT APPLICATION NUMBER: US/10/366,125
CURRENT FILING DATE: 2003-02-12
PRIOR PILING DATE: 2002-02-12
PRIOR PLING DATE: 2002-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-908-711-78

US-09-908-711-78

Sequence 78, Application US/09908711

Patent No. US20020045230A1

GRNERAL INFORMATION:

TITLE OF INVENITION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PA128

CURRENT APPLICATION NUMBER: US/09/908,711

CURRENT APPLICATION NUMBER: US/09/908,711

FRIOR APPLICATION NUMBER: US/09/908,711

PRIOR FILING DATE: 2001-01-17

PRIOR APPLICATION NUMBER: US/01/0134

PRIOR APPLICATION NUMBER: US/01/0134

PRIOR APPLICATION NUMBER: US/01/0134

PRIOR PILING DATE: 2001-01-17

PRIOR PILING DATE: 2001-01-17

PRIOR PILING DATE: 2001-01-17

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PRIOR PELING DATE: 2001-01-17
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                                                                  Score 48; DB 15; Length 25;
Pred. No. 0.46;
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                                                                                                                              0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                          Sequence 19, Application US/10366125
Publication No. US20030228259A1
GENERAL INFORMATION:
                                                                       Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapiens
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US-09-908-711-78
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                                                                                                                                                                                                                                                                                                                                                            US-10-366-125-19
        ; ORGANICALI
US-10-366-125-11
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TITLE OF INVENTION: MEASUREMENT OF BIOSYNTHESIS AND BREAKDOWN RAIES OF
TITLE OF INVENTION: MEASUREMENT OF BIOSYNTHESIS AND BREAKDOWN RAIES OF
TITLE OF INVENTION: BALLEL INCORPORATION INTO METABOLIC DERIVATIVES AND
TITLE OF INVENTION: CATABOLITIC PRODUCTS
TITLE OF INVENTION: CATABOLITIC PRODUCTS
CURRENT APPLICATION NUMBER: US/10/366,125
CURRENT APPLICATION NUMBER: US/10/366,125
PRIOR PILING DATE: 2002-02-12
PRIOR FILING DATE: 2002-02-12
                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Byre, David R.
TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS
FILE REFERENCE: WROS-1-1320
CURRENT APPLICATION NUMBER: US/10/615,959
CURRENT APPLICATION NUMBER: US/10/009,999A
PRIOR APPLICATION NUMBER: US/10/009,999A
PRIOR PELING DATE: 2003-01-22
PRIOR PELING DATE: 1999-12-10
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
PRIOR PELING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: US 60/142,274
PRIOR PELING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
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PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PRIOR PRIOR NUMBER: US 60/142,675
PRIOR FILING DATE: 1999-07-07
PRIOR PRIOR PRIOR DATE: 1999-07-07
PRIOR PRIOR PRIOR DATE: 1999-07-07
PRIOR PRIOR PRIOR DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 45
SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MISC_FEATURE
OTHER INFORMATION: synthetic peptide corresponding to carboxy-terminal
OTHER INFORMATION: telopeptide sequence of human type III collagen
US-10-615-959-43
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 25
TYPE: PRT
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US-10-366-125-11
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US-10-615-959-43
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                                                                                                                                                                                                                       Sequence 226, Application US/09918715
Sequence 226, Application US/09918715
Publication No. US20030017157A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Renneth Kinzler
TILLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: 06/222,599
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR PELING DATE: 2000-08-11
PRIOR PELING DATE: 2000-08-11
PRIOR PELING DATE: 2000-08-11
PRIOR PELING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: PESTSEQ for Windows Version 3.0
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APPLICANT: Sherman-Baust, Cheryl A.
APPLICANT: Pizer, Ellen S.
APPLICANT: Pizer, Ellen S.
APPLICANT: Hough, Colleen D.
TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER FILE REFERENCE: 14014,036902
CURRENT APPLICATION NUMBER: US/10/257,021
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: PCT/US01/10947
PRIOR APPLICATION NUMBER: 60/194,336
PRIOR APPLICATION NUMBER: 60/194,336
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 147
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7: SEQ ID NOS: 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 72, Application US/10257021
Publication No. US20030211498A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 9; Conservative
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Matches 9; Conservative
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51 IGGEKAGGF 59
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; ORGANISM: Homo sapiens
US-09-918-715-226
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ORGANISM: Homo sapiens
US-10-257-021-72
1 IGGEKAGGF 9
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US-09-918-715-226
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CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
LOCATION: (4)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-908-711-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILLING DATE: 2001-01-7
PRIOR FILING DATE: 2001-01-7
PRIOR APPLICATION NUMBER: 09/764,902
PRIOR FILING DATE: 2001-01-7
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR PELICATION NUMBER: 09/764,870
PRIOR FILING DATE: 2001-01-17
PRIOR PELICATION NUMBER: 09/764,890
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,882
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,896
PRIOR FILING DATE: 2001-01-17
PRIOR PELICATION NUMBER: 09/764,864
PRIOR FILING DATE: 2001-01-17
PRIOR PELICATION NUMBER: 09/764,864
PRIOR FILING DATE: 2001-01-17
PRIOR PELICATION NUMBER: 09/764,864
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,866
PRIOR FILING DATE: 2001-01-17
PRIOR PELICATION NUMBER: 09/764,866
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PRIOR PELICATION NUMBER: 09/764,866
PRIOR FILING DATE: 2001-01-17
PRIOR PELICATION NUMBER: 09/764,867
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                                   PRIOR APPLICATION NUMBER: USOJ. 01139
PRIOR FILING DATE: 2001-01-1/
PRIOR FILING DATE: 2001-01-1/
PRIOR PELICATION NUMBER: 09/764,869
PRIOR FILING DATE: 2001-01-1/
PRIOR APPLICATION NUMBER: USOJ. 01340
PRIOR FILING DATE: 2001-01-1/
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RAPPLICATION NUMBER: US01/01320
RETLING DATE: 2001-01-17
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ORGANISM: Homo sapiens
FEATURE:
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US-10-357-851-3
US-10-357-851-3
Sequence 3, Application US/10357851
Sequence 3, Application US/10357851
Sequence 3, Application US/20040151731A1
GENERAL INFORMATION:
THE GENERAL INFORMATION:
TITLE OF INVENTION: T-Lymphocyte Reactivity with Collagen in Aortic Tissue of TITLE OF INVENTION: Abdominal Aortic Aneurysm Patients
TITLE OF INVENTION: Abdominal Aortic Aneurysm Patients
TITLE OF INVENTION: Abdominal Aortic Aneurysm Patients
CURRENT APPLICATION NUMBER: US/10/357,851
CURRENT FILING DATE: 2003-02-04
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1466
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; Sequence 3, Application US/10358024
; Publication No. US20040151732A1
; GENERAL INFORMATION:
    APPLICANT: Jicha, Douglas L.
    APPLICANT: Jicha, Douglas L.
    APPLICANT: Jicha, Stephen
; TITLE OF INVENTION: Methods and Compositions Involving Blood
    TITLE OF INVENTION: T-Lymphocytes Reactivity with Collagen
; TITLE OF INVENTION: T-Lymphocytes Reactivity with Collagen
; TURRENT APPLICATION UNUMBER: US/10/358,024
; CURRENT FILING DATE: 2003-02-04
; CURRENT FILING DATE: 2003-02-04
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1466
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                   FILE REFERENCE: MPMO1-0292RNM

FILE REFERENCE: MPMO1-0292RNM

CURRENT APPLICATION NUMBER: US/10/301,822

CURRENT FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US 60/339,971

PRIOR FILING DATE: 2001-12-10

PRIOR FILING DATE: 2001-03-05

PRIOR FILING DATE: 2002-03-05

PRIOR APPLICATION NUMBER: US 60/361,978

PRIOR APPLICATION NUMBER: US 60/361,978

PRIOR APPLICATION NUMBER: US 60/361,978

PRIOR PILING DATE: 2002-05-20

NUMBER OF SEQ ID NOS: 228

SEQ ID NO 33

LENGTH: 1466

TYPE: PRI

TYPE: PRI

CRGANISM: Homo Sapiens

US-10-301-822-33
TITLE OF INVENTION: THERAPY OF COLON CANCER
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Best Local Similarity 100.
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ORGANISM: Homo Sapiens
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APPLICANT: BASE LI., KOOSET C.
APPLICANT: HOTCODAGY, Gabriel N.
APPLICANT: PUSZTAI, Lajos
APPLICANT: MAIN, CHOTCODAGY, Gabriel N.
APPLICANT: MAIN, CHOTCODAGY, Gabriel N.
APPLICANT: MAIN, Gordon B.
TITLE OF INVENTYON: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, TITLE OF INVENTYON: COMPOSITIONS, AND THERAPY OF BREAST CANCER
TITLE OF INVENTYON: WOMBER: US/10/17,293
CURRENT PELING DATE: 2002-06-21
PRIOR PAPLICATION NUMBER: US 60/299,887
PRIOR FILING DATE: 2001-06-21
PRIOR PAPLICATION NUMBER: US 60/301,572
PRIOR PAPLICATION NUMBER: US 60/305,501
PRIOR FILING DATE: 2001-09-25
PRIOR PAPLICATION NUMBER: US 60/305,501
PRIOR PAPLICATION NUMBER: US 60/305,505
PRIOR PAPLICATION NUMBER: US 60/305,505
PRIOR PAPLICATION NUMBER: US 60/305,505
PRIOR PILING DATE: 2001-09-25
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SOFTWARE PRESENTED TO NINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Berger, Alison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Ramatkar, Shubhangi
APPLICANT: Ramatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Publication No. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                             Sequence 68, Application US/10177293 Publication No. US20030124128A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       Xu, Yongyao
Hoersch, Sebastian
Monahan, John
Meyers, Rachel E.
Bast Jr., Robert C.
                                                                                                                                                                                     APPLICANT: Lillie, James
APPLICANT: Glatt, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Gannavarpu, Manjula
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Mertens, Maureen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
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US-10-177-293-68
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US-10-301-822-33
                                                     RESULT 8
US-10-177-293-68
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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(SENDER 1615-959-40)

(SEQUENCE 40, Application US/10615959)

(SENDERL INCORMATION:

(TILL OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS

(TILLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS

(TILLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS

(TILLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS

(TURRENT PELLOR DATE: 2003-01-08

(TURRENT PILLOR DATE: 2003-01-02

(TURRENT PILLOR DATE: 2003-01-02

(TURRENT PILLOR DATE: 1999-12-10

(TURRENT PILLOR DATE: 1999-12-10

(TURRENT PILLOR DATE: 1999-12-10

(TURRENT PILLOR DATE: 1999-06-17

(TURRENT PILLOR DATE: 1999-07-02

(TURRENT PILLOR DATE: 1999-07-07

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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87.5%; Score 42; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels
      Sequence 12, Application US/10402072A
Publication No US20040018592A1
GENERAL INFORMATION:
APPLICANT: Bell, Marcum P.
APPLICANT: Bell, Marcum P.
APPLICANT: Bellarek, James W.
APPLICANT: Seeley, Todm W.
TITLE OF INVENTION: BOVINE COLLAGENS AND GELATINS:
FILE REFERENCE: FP046.2 CON
CURRENT APPLICATION NUMBER: US/10/402,072A
CURRENT FILING DATE: 2003-03-26
FRIOR APPLICATION NUMBER: US 09/709,700
FRIOR PILING DATE: 2000-11-10
NUMBER OF SEQ 1D NOS: 72
SOFTWARE: Patentin version 3.2
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1208 VGGEKAGGF 1216
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IGGEKAGGF 9
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ORGANISM: Sus scrofa
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Best Local Similarity 100.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 0; Indels 0
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88.9%; Pred. No. 34;
tive 1; Mismatches 0; Indels (
                                                                                                                                                                  0; Indels
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Publication No. US20040005663A1
GENERAL INFORMATION:
APPLICANT: Bell, Marcum P.
APPLICANT: Bell, Marcum P.
APPLICANT: Bell, Marcum P.
TILE OF INVENTION: PORCINE COLLAGENS AND GELATINS
FILE REFERENCE: FP0402.3 COM
CURRENT APPLICATION NUMBER: US/10/402,089
CURRENT FILING DATE: 2003-03-05
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 72
SOFFWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                   US-10-734-564-103
Sequence 103, Application US/10734564
Sequence 103, Application US/10734564
Sequence 103, Application US/10734564
GENERAL INCRNATION:
TITLE OF INVENTION: Detection Methods Using TIMPL
TITLE OF INVENTION: Detection Methods Using TIMPL
CURRENT PEDLICATION NUMBER: US/10/734,564
CURRENT FILING DATE: 2003-12-12
NUMBER OF SEQ ID NOS: 138
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 103
LENGTH: 1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                    1208 İĞĞEKAĞĞF 1216
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1208 VGGEKAGGF 1216
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; ORGANISM: Homo sapiens
US-10-734-564-103
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: LENGTH: 1466

: TYPE: PRT

; ORGANISM: SUS SCROFA

US-10-402-089-12
ORGANISM: Homo Sapien
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Best Local Similarity
Matches 9, Conserv
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US-10-402-072A-12
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             ; UKGANIGH. III.
US-10-358-024-3
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Search completed: September 18, 2004, 04:56:13 Job time : 43.7059 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

September 18, 2004, 04:02:05; Search time 10.9412 Seconds (without alignments) 79.125 Million cell updates/sec

US-10-615-959-41 48 1 IGGEKAGGF 9 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* PIR 78:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ES	Description	)	Corragen arbina 1.	י) ו מלת למ הפסמל ( סמ	nrobable Southern	hypothetical prote	hypotherical prote	glycine cleavade	hypotherical 43.7K	hypothetical prote		keratin, 65K rvne	X3.	7	formylmethanofuran	formylmethanofuran	hypothetical prote	N-anetrial processing proce	D-160mulance I manga dah	hypothetical prote	hypothetical prote	σ		hynotherical prote		no no managem	1)	4 -	٦,	CODSERVED bynother
SUMMARIES	ID	CGHU7L	S41067	559856	G72777	AG1031	AH2756	G97537	S56535	E91287	H86128	A29666	S42629	S14998	H69074	S57457	E84505	AF1720	S55482	T24323	B87269	A45268	AE2301	875539	G72282	\$28081	B24785	8463	17	₹#
	DB	-	~	7	7	7	7	7	N	N	7	7	N	7	N	7	7	~	7	7	~	~	7	7	7	~	~	~	7	7
	Length	1466	636	1464	383	476	357	379	404	404	404	629	629	191	270	270	324	375	382	440	457	468	475	490	909	1009	1028	1440	165	9
æ	Query	100.0	91.7	91.7	79.2	77.1	75.0	75.0	75.0	75.0	75.0	75.0	75.0	72.9	72.9	72.9	72.9	72.9	72.9	72.9	72.9	72.9	72.9	72.9	72.9	72.9	72.9	72.9	70.8	70.8
	Score	48	44	44	38	37	36	36	36	36	36	36	36	35	35	35	35	35	35	35	35	32	35	35	35	35	35	35	34	34
	Result No.	-	7	e	4	S	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	G18-1.2-G1hvdro-1	hypotherical prote	hypothetical prote	Cell wall-associat	phosphoglicomitase	probable phosphogl	phosphoglicomitaes	Carboxy]esterase /	Carboxy]esterase	carboxylesterase (	hypotherical profe	hynothetical prote	F28G4 21 Arotein		ribonucleoside-dip
B36724	T31264	T33925	T14636	G96937	C84378	F82302	C70345	S62788	S71597	S10367	T32923	T02366	H86309	C82077	WMBEB1
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240	266	276	324	371	457	470	499	561	561	265	809	644	718	948	1137
70.8	70.8	70.8	70.8	70.8	70.8	70.8	70.8	70.8	70.8	70.8	70.8	70.8	70.8	70.8	70.8
34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	<b>4</b> .5

# ALIGNMENTS

_	RESULT 1	
	CGHU7L	
	collagen alpha 1(III) chain precursor - human	
	N,Alternate names: procollagen alpha 1(III) chain	
	C; Species: Homo sapiens (man)	
	C;Date: 24-Apr-1984 #sequence revision 01-Sep-1995 #text change 21-Jul-2000	
	C;Accession: S05272; S04642; PE0011; S01726; S04887; A90399; A94562; I51868; S59511; A904	
	R, Prockop, D.J.	
	submitted to the EMBL Data Library, February 1989	
_	A; Reference number: S05272	
	A; Accession: S05272	
_	A;Status: preliminary	
	A;Molecule type: mRNA	
	A;Residues: 1-1240,'V',1242-1466 <prc></prc>	
	A; Cross-references: EMBL: X14420; NID: 0330057; PIDN: CAA32583.1; PID: 030058	
	R,Ala-Kokko, L.; Kontusaari, S.; Baldwin, C.T.; Kuivaniemi, H.; Prockon, D.J.	_
	Biochem. J. 260, 509-516, 1989	_
_	A, Title: Structure of cDNA clones coding for the entire prepro-alphal (TII) chain of human	
	erences.	_
	A; Reference number: S04642; MUID:89350838; PMID:2764886	_
_	A; Accession: S04642	_
	A;Molecule type: mRNA	
_	A;Residues: 1-1196 <ala></ala>	
	A; Cross-references: EMBL:X14420; NID: 330057; PIDN: CAA32583.1; PID: 730058	
	A; Note: the complete sequence is not shown	
_	R;Benson-Chanda, V.; Su, M.W.; Weill D.; Chu, M.T Ramirez E	_
	1 (3) 11 11 11 11 11 11 11 11 11 11 11 11 11	

Gene 78, 255-265, 1989 A/Title: Cloning and analysis of the 5' portion of the human type-III procollagen gene A/Reference number: PE0011; MUID:89378752; PMID:2777083

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A,Accession: PEGO11
A,Modecule type: DNA
A,Residues: 1-176 < ABNA
A,Cross-references: GB:MA26939; NID:g180813; PIDN:AAA52040.1; PID:g180814
R,Toman, P. D.; R.Acca, G.A.; de Crombrugghe, B.
Mucleic Acids Res. 16, 7201, 1988
A,Title: Nucleotide sequence of a CDNA coding for the amino-terminal region of human prep

A,Accession: S01726
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Residues: 1-170 <TOM
A,Cross-references: EMBL:X07240, NID:g30060, PIDN:CAA30229.1, PID:g30061
A,Note: the authors translated the codon CAG for residue 154 as His
R;Janeczko, R.A.; Ramirez, F.
R;Janeczko, R.A.; Ramirez, F.
A;Title: Nucleotide and amino acid sequences of the entire human alpha-1 (III) collagen.
A;Reference number: S04887; MUID:89386015; PMID:2780304

A,Molecule type: mRNA A;Residues: 149-163, G',164-240, D',242-471, D',473-487, L',489,'S',491-613,'Y',615-634,' A;Cross-references: EMBL:X15332; NID:g29545; PIDN:CAA33387.1; PID:g930045 A;Note: the authors' translation of residues 905-932 is inconsistent with the nucleotide R;Seyer, J.M.; Kang, A.H.

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A,Status: translated from GB/EMBL/DDBJ
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Biochemistry 20, 2621-2627, 1981
A,Title: Covalent structure of C
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A; Molecule type: DNA
A; Residues: 537-605 < LEE>
A; Cross-references: GB:MS9312; NID:g180815; PIDN:AAA52041.1; PID:g180816
A; Cross-references: GB:MS9312; NID:g180815; PIDN:AA52041.1; PID:g180816
R; Seyer, J.M.; Mainardi, C.; Kang, A.H.
Biochemistry 19, 1583-1589, 1980
A; Title: Covalent structure of collagen: amino acid sequence of alphal (III)-CB5 from ty A; Recence number: A90438; MUD:80198282; PMID:6246925
A; Accession: A90438; MUD:80198282; PMID:6246925
A; Rccession: A90438; MUD:91009133; PMID:2145268
A; Rccession: A90803
A; Reference number: A38303; MUD:91009133; PMID:2145268
A; Residues: B61-1015 < COL>
A; Title: A base substitution at a sphice site in the COL3A1 gene causes exon skipping an A; Rocele type: mRNA
A; Residues: B61-1015 < COL>
A; Title: A base substitution at a sphice site in the COL3A1 gene causes exon skipping an A; Rocele type: mRNA
A; Residues: B61-1015 < COL>
A; Title: A base substitution at a sphice of the colabal gene causes are a sphice with 942-977 spliced out from a patient with Ehlers-Danlos syn Nucleic Acids Res 16, 2337, 1988
A; Nocle: A mutant sequence with 942-977 spliced out from a patient with Ehlers-Danlos syn Nucleic Acids Res 16, 2337, 1988
A; Nocle: A mutant Sequence All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; All A; 
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A;Reference number: IS1868
A;Reference i IS1868
A;Refeus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 186-194 < MIL>
A;Cross-references: GB:862925; NID:9386425; PIDN:AAD13937.1; PID:94261637
B;Chiodo, A.A.; Sillence, D.O.; Cole, W.G.; Bateman, J.F.
Biochem. J. 311, 399-943, 1995
A;Title: Abnormal type III collagen produced by an exon-17-skipping mutation of the COL3
A;Reference number: S59511; MUID:96067614; PMID:7487954
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A;Residues: 'V',169-225,229-232,'P',234-292,'D',294-398 <SEX1>
A;Experimental source: liver
A;Note: sequence corrected by A94562; attachment of 2-O-alpha-D-glucosyl-O-beta-D-galact
R;Seyer, J.M.
submitted to the Atlas, December 1977
A, Title: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptide A, Reference number: A90399; MUID:77134724; PMID:557335
A, Accession: A90399
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A;Accession: A94562
A;Accession: A94562
A;Molecule type: protein
A;Experimental source: liver
A;Experimental source: liver
A;Note: author submitted corrections to A90399
R;Midewicz, D.M.; Witz, A.M.; Smith, A.C.; Manchester, D.K.; Waldstein, G.; Byers, P.H. Am. J. Hum. Genet. 53, 62-70, 1993
A;Title: Parental somatic and germ-line mosaicism for a multiexon deletion with unusual
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A, Residues: 302-423 < CHI>
A, Residues: 302-423 < CHI>
B, Residues: 302-423 < CHI>
B, Residues: 302-423 < CHI>
B, Residues: 302-423 < CHI>
B, Seyer, J.M.; Kang, A.H.
Biochemistry 17, 3404-3411, 1978
B, A, Miller Covalent structure of collagen: amino acid sequence of five consecutive CNBr I
A, Accession: A90414; MUID:79000343; PMID:687591
A, Molecule type: protein
A, Molecule type: protein
A, Molecule type: protein
A, Molecule type: Superir Furga,
B, Esperimental source: 11ver
B, Liee, B.; Vitale, E.; Superir Furga, A.; Steinmann, B.; Ramirez, F.
J. Biol. Chem. 266, 5256-5259, 1991
A, Pitle: G to T transversion at position +5 of a splice donor site causes skipping of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the stat
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Title: Human pro alphal(III) collagen: cDNA sequence for the 3' end,
Reference number: S02119; MUID:88189827; PMID:3357782
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A;Status: translated from GB/EMBL/DDBJ
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A; Molecule type: protein
A;Reaidues: 965-979, A', 981-984, 'PS', 987, 'QN', 990-1096, 'P', 1098-1152, 'AT', 1155, 'S', 1157-3
A;Experimental source: liver
A;Experimental source: liver
Nucleic A;Experimental source: liver
Nucleic A;Experimental source: liver
Nucleic A;Experimental source: liver
A;Title: Molecular cloning and carboxyl-propeptide analysis of human type III procollager
A;Reference number: A93551; MUID:85087944; PMID:6096827
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1;Residues: 1065-1155,'P',1157-1466 <LOI>
1;Cross-references: EMBL:X01655; EMBL:X01742; NID:929584; PIDN:CAA25821.1
2;Miskulin, M.; Dalgleish, R.; Kluve-Beckerman, B.; Rennard, S.I.; Tolstoshev, P.; Brantl
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A.Fitle: Human type III collagen gene expression is coordinately modulated with the type
A,Reference number: I52393; MUID:86187804; PMID:3754462
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A; Residues: 1161-1200 <MIS>
A; Residues: 1161-1200 <MIS>
A; Cross-references: 1161-1200 <MIS>
A; Cross-references: 1200 <MIS>
R; Cross-references: 1200 <MIS>
B; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C.
Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
A; Title: Human alpha 1(III) and alpha 2(V) procollagen genes are located on the long arm A; Reference number: 159025; MUID: 85116505; PMID: 3858826
A; Accession: 179359
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A;Cross-references: GB:M10615; GB:M10793; GB:M10794; GB:M10795; GB:M10796; GB:M10797; GB
A;Experimental source: liver
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A;Map position: 2q31-2q31
A;Introns: 27/1; 94/3; 111/3; 149/3; 176/3; 554/3; 587/3; 1175/3; 1275/1; 1337/3; 1418/3
A;Introns: 27/1; 94/3; 111/3; 149/3; 176/3; 554/3; 587/3; 1175/3; 1275/1; 1337/3; 1418/3
A;Introns: 27/1; 94/3; 111/3; 149/3; 176/3; 554/3; 587/3; 1175/3; 1275/1; 1337/3; 1418/3
A;Introns: 27/1; 94/3; 111/3; 149/3; 110/3; 160/2; defects in this gene can result in Ehlers-Dan C;Complex: type III collagen is a homotrimer of monomers initially linked by disulfide be er of their length, is formed with desmosine cross-links made from lysine and allysine r
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F; 1-31/Domain: amino-terminal propeptide #status predicted <PRO>
F; 1-154/Domain: von Willebrand factor type C repeat homology <WAC>
F; 1-191/Domain: von Willebrand factor type C repeat homology cWAC>
F; 1-154/Region: amino-terminal nonhelical telopeptide
F; 1091-1093/Region: carboxyl-terminal nonhelical telopeptide
F; 1197-1221/Region: carboxyl-terminal nonhelical telopeptide
F; 1221-1466/Domain: carboxyl-terminal propeptide #status predicted <CPR>
F; 1239-1466/Domain: fibrillar collagen carboxyl-terminal homology <PCC>
                                                                                                                                                                                                                                                                                                                   A, Title: Covalent structure of collagen: amino acid sequence of alphal (III)-CB9 from tyf A, Reference number: A90446; MUID:81208139; PMID:7016180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ); Comment: Prolines and lysines at the third position of the tripeptide repeating unit 3-hydroxylated. About 15% of the lysines are 5-hydroxylated and some are subsequently
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A,Residues: 1165-1196 <EMA>
A,Cross-references: GB:M11134; NID:g180417; PIDN:AAA52004.1; PID:g180418
R;Chu, M.L.; Well, D.; de Wet, W.; Bernard, M.; Sippola, M.; Ramirez, F.
J. Biol. Chem. 260, 4157-4363, 1965
A;Title: Isolation of cDNA and genomic clones encoding human pro-alphal(III)
A;Reference number: A92516; MUID:85157600; PMID:2579949
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 950-1018,'Y',1020-1183,'S',1185-1466 <WAN>
A;Cross-references: EMBL:X06700; NID:g30053; PIDN:CAA29886.1; PID:g30054
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III and IX collagen mRNAs.

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hypothetical protein STY4577 [imported] - Salmonella enterica subsp. enterica serovar Tyr
C;Species: Salmonella enterica subsp. enterica serovar Typhi
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                         A;Accession: S59856
A;Molecule type: DNA
A;Residues: 1-1464 <TOM>
A;Cross-references: EMBL:X52046
R;Toman, D.
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Matches
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 13-Aug-1999
C;Accession: S41067; A29965; S31924
R;Glumoff, V.; Mackelae, J.K.; Vuorio, E.
Biochim. Biophys. Acta 12.7, 41-48, 1994
A;Title: Cloning of CDNA for rat pro alpha-1(III) collagen mRNA. Different expression pa A;Reference number: S41067; MUID:94114571; PMID:8286415
A;Reference number: S41067
A;Residues: I-636 «GLUS
A;Residues: L-636 «GLUS
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A;Residues: L-636 » «GL
F;24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted F;153-154/Cleavage site: Pro-Gln (procollagen N-endopeptidase) #status predicted F;154/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted F;161,1212/Modified site: allysine (Lys) #status predicted F;263,284,860,977,1106/Modified site: 5-hydroxylysine (Lys) #status experimental F;263,284,1094/Modified site: 5-hydroxylysine (Lys) #status experimental F;584,1094/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental F;584,1094/Modified site: 67-hydroxylysine (Lys) (partial) #status experimental F;948-949/Cleavage site: Gly-11e (Collagenase) #status sxperimental F;1106/Binding site: carbohydrate (Lys) (covalent) #status predicted
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C;Species: Mus musculus (house mouse)
C;Date: 10-Apr-1996 #sequence revision 19-Apr-1996 #text_change 13-Aug-1999
C;Date: 10-Apr-1996 #sequence revision 19-Apr-1996 #text_change 13-Aug-1999
C;Accession: S59856; S5120; Si6373
R;Toman, P.D.; de Crombrugghe, B.
Gene 147, 161-168, 1994
A;Title: The mouse type-III procollagen-encoding gene: genomic cloning and complete DNA
A;Reference number: S59856; MUID:95011609; PMID:7926795
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C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
C;Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix
F;408-636/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
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A,Accession: A29905
A,Accession: A29905
A,Accession: 308-48
A,February, Pebruary 1993
A,Cross-references: GB.M21354; NID:g203500, PIDN:AAA40942.1; PID:g203501
B,Cross-references: Data Library, February 1993
A,Reference number: S31924
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Best Local Similarity 100.0%;
Matches 9; Conservative (
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Best Local Similarity 77.8
Matches 7; Conservative
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378 VGGEKSGGF 386
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A;Molecule type: mRNA
A;Residues: 2-636 <GL2>
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Aintrons: 29/1; 95/3; 112/3; 150/3; 175/3; 193/3; 211/3; 229/3; 247/3; 265/3; 283/3; 298
58/3; 673/3; 706/3; 742/3; 760/3; 778/3; 796/3; 814/3; 850/3; 868/3; 868/3; 868/3; 976/3; 6.5 superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology; C; Keywords: coiled coll; extracellular matrix
F;1-24/Domain: signal sequence #status predicted <SIG>F;25-154/Domain: propeptide #status predicted <PRO>F;32-92/Domain: von Willebrand factor type C repeat homology <VWC>F;32-92/Domain: von Willebrand factor type C repeat homology <VWC>F;1236-1464/Domain: tibrillar collagen carboxyl-terminal homology <FCC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Aeropyrum pernix
C;Date: 20-hug-1999 #sequence_revision 20-hug-1999 #text_change 20-hug-1999
C;Accession: G72777
R;Kawarabayasi, Y; Hino, Y:; Horikawa, H; Yamazaki, S; Haikawa, Y:; Jin-no, K.; Takaha awa, H; Takamiya, M.; Masuda, S:; Funahashi, T:; Tanaka, T:; Kudoh, Y:; Yamazaki, J:; K. Axamiya, A:1115: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyru A;Accession: G72777
A;Accession: G72777
A;Status: preliminary
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A;Experimental source: strain K1
C;Genetics:
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                                                                                       A; Cross-references: EMBL:X57983; NID:g50476; PIDN:CAA41048.1; PID:g50477
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Pred. No. 8.3;
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0; Mismatches
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Matches 7; Conservative
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1442-1464 <MET>
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Gaps

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Length 379; Indels

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hypothetical 43.7K protein (fecI-fimB intergenic region) - Escherichia coli (strain K-12 N,Alternate names: hypothetical protein f404 C;Species: Escherichia coli (5,5pecies: Escherichia coli (5,5pecies: Escherichia coli (5,5pace: 28-0ct-1995 #sequence_revision 03-Nov-1995 #text_change 01-Mar-2002 C;Accession: 856535; H6524 R;Burland, V; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R. Nucleic Acids Res. 23, 2105-2119, 1995 A;Aritle: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.6 A;Reference number: 856315 A;Reference number: 856315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:U14003; NID:g1263172; PIDN:AAA97206.1; PID:g537151
A;Cross-references: EMBL:U14003; NID:g1263172; PIDN:AAA97206.1; PID:g537151
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co.A.; Rose, D.J.; Mau, B.; Shao, Y.
A;R Rose, D.J.; Mau, B.; Shao, Y.
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
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                                      A;Molecule type: DNA
A;Reaiduee: 1-379 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK87256.1; PID:g15156544; GSPDB:GN00169
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64;
                                                                                                                                                                                                                                                                                                                                                                         75.0%; Score 36; DB 75.0%; Pred. No. 64; cive 1; Mismatches
                                                                                                                                                                                                                                                                                            C;Superfamily: aminomethyltransferase
                                                                                                                                                                                                   A;Gene: AGR C 2701
A;Map positIon: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                           llarity 75.0%;
Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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Matches 6; Conserv
            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                              C; Genetics:
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AH2756
hypothetical protein gcvT [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Decies: Agrobacterium tumefaciens
C;Decies: Agrobacterium tumefaciens
C;Decies: Agrobacterium tumefaciens
C;Decies: Agrobacterium tumefaciens
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C;Decies: Agrobacterium tumefaciens
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C;Decies: Agrobacterium tumefaciens
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
R;Wood, D.W.; Setubal, J. S.; Zang, S.; Zang, S.; Zang, S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, J. S.; Zang, 
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(497537
glycine cleavage system protein T2 (PA2442) [imported] - Agrobacterium tumefaciens (straglycine cleavage system protein T2 (PA2442) [imported] - Agrobacterium tumefaciens G;Species: Agrobacterium tumefaciens
C;Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: G97537
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MuID:21608551; PMID:11743194
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: Ad031
R;Parkill, J; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, A.; Moule, S.; O'Gaora, P.
Nature 413, 484-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Millors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AG1031
A;Status: preliminary
A;Residues: 1-476 cPAR>
A;Residues: 1-476 cPAR>
A;Coosg_references: GB:AL513382; PIDN:CAD09352.1; PID:g16505352; GSPDB:GN00176
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Best Local Similarity 75.0%; Score 36; DB 2; Length 357;
Best Local Similarity 75.0%; Pred. No. 60;
Matches 6; Conservative 1; Mismatches 1: Indels
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211 VGGKKAGG 218
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248 GGEREGGF 255
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Matches 6; Conserv
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A;Gene: STY4577
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                         Cispecies: Escherichia coli
Cipacies: 18-011-2001 #sequence_revision 18-011-2001 #text_change 18-011-2001
CiAccession: E91287
CiAccession: E91287
CiAccession: Faunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Yokoyama, K.; Han, C.G.
Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
NA, Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and geno
A, Reference number: A99629; MUID:21156231; PMID:11258796
A, Accession: E91287
A, Accession: E91287
A, Residues: 1-404 <HAY>
hypothetical protein ECS5269 (imported) - Escherichia coli (strain 0157.H7, substrain
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J. Cell Sci. 105, 303-316, 1993
A;Title: A 300 bp 5'-upstream sequence of a differentiation-dependent rabbit K3 keratin c
A;Reference number: S42629; MUID:94013038; PMID:7691837
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R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; F;Smith, D.R.; Boucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; F;Smith, D.R.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Tille: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functi
A;Reference number: A69000; MUID:98037514; PMID:9371463
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                                                                                                                                                                                                                             C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C;Accession: S42629
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C;Dates: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C;Accession: S14998
R;Goping, 1.S.; Frappier, J.R.H.; Walden, D.B.; Atkinson, B.G.
A;Title: Sequence, identification and characterization of cDNAs encoding two A;Reference number: S14998
A;Reference number: S14998
A;Reference revpe: man A
A;Reference: Comman A
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C.Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Sep-1999
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C;Superfamily: cytoskeletal keratin
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Pred. No. 1e+02;
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C;Superfamily: alpha-crystallin
C;Keywords: heat shock; stress-induced protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heat shock protein 18 (clone c9) - maize
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85.7%;
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Matches 6; Conservative
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-404 cSTO>
A;Cross-references: GB:AE005174; NID:g12519317; PIDN:AAGS9492.1; GSPDB:GN00145; UWGP:Z59
A;Experimental source: strain 0157:H7, substrain EDL933
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C;Date: 31-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 20-Apr-2001
C;Date: 31-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 20-Apr-2001
C;Accession. A29666
R;Kilnge, E.M.; Sylvestre, Y.R.; Freedberg, I.M.; Blumenberg, M.
J. Mol. Evol. 24, 319-329, 1987
A;Title: Exolution of keratin genes: different protein domains evolve by different pathw A;Reference number: A29666; MUID:87254239; PMID:2439698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein yjhT [imported] - Escherichia coli (strain 0157:H7, substrain EDL93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Bscherichia coli

C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C; Accession. H86128

R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

Nature 409, 529-533, 2001

A; Title: Genome sequence of enterchemorrhagic Escherichia coli 0157:H7.

A; Reference number: A85480; MUID:21074935; PMID:11206551
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A;Cross-references: GB:BA000007; PIDN:BAB38692.1; PID:g13364747; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC85269
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C;Superfamily: cytoskeletal keratin
C;Keywords: coiled coil
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Pred. No. 68;
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A,Gene: yjhT
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A;Residues: 1-270 <WTH>
A;Residues: 1-270 <WTH>
A;Cross-references: GB:AE000916; GB:AE000666; NID:g2622674; PIDN:AAB86032.1; PID:g262268
A;Cross-references: GB:AE000916; GB:AE000666; NID:g2622674; PIDN:AAB86032.1; PID:g262268
C;Genetics: C;Genetics: Afgeriant Bource: Strain Delta H
C;Genetics: C;Genetics: Comylmethanofuran dehydrogenase chain C
C;Superfamily: formylmethanofuran dehydrogenase chain C
C;Keywords: iron-sulfur protein; metalloprotein; oxidoreductase; tungsten
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A;Residues: 1-270 <HOC>
A;Cross-references: EMBL:X87970; NID:g1890205; PIDN:CAA61214.1; PID:g1890211
A;Experimental source: strain Marburg, DSM 2133
C;Genetics:
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A;Gene: fwdC C;Complex: heterotetramer of A (see PIR:SS7456), B (see PIR:SS7458), C, and D (see PIR:S C;Superfamily: formylmethanofuran dehydrogenase chain C C;Keywords: heterotetramer; iron-sulfur protein; metalloprotein; oxidoreductase; tungste

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Query Match 72.9%; Score 35; DB 2; Length 270; Best Local Similarity 75.0%; Pred. No. 70; Matches 6; Conservative 1; Mismatches 1; Indels

Search completed: September 18, 2004, 04:30:51 Job time : 11.9412 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 18, 2004, 03:48:54; Search time 6.70588 Seconds (without alignments) 69.884 Million cell updates/sec Run on:

US-10-615-959-41 48 1 IGGEKAGGF 9 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	1 homo sapien	1 rattu	1 mus musculu	1 escherichia	5 homo sapien		_	<u> </u>	0 schizosacch					5 streptomyce		0 rattus norv	3 rattus norv	3 herpes simp		5 murine coro		6 thermoplasm	•		5 methanosarc	0 bacteriopha	-			9 craterostiq		8 escherichia	1 schizosacch
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34 35	36 37	8 6 8 6	40	. 4. 4 . 2 4.	4.	45

# ALIGNMENTS

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SEQUENCE OF 1176-1466 FROM N.A.
MEDLINB=85157600; PubMed=2579949;
Chu M.-L., Weill D., de Wet W.J., Bernard M.P., Sippola M., Ramirez F.;
"Isolation of cDNA and genomic clones encoding human pro-alpha 1
(III) collagen. Partial characterization of the 3' end region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kuivaniemi H., Tromp G., Prockop D.J.;
Kuivaniemi H., Tromp G., Prockop D.J.;
"Mutations in fibrillar collagens (types I, II, III, and XI), fibrilassociated collagen (type IX), and network-forming collagen (type X) cause a spectrum of diseases of bone, cartilage, and blood vessels.";
Hum. Mutat. 9:300-315(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-88303366, PubMed=3405773;
Toman D., Ricca G., de Crombrugghe B.;
Nucleotide sequence of a cDNA coding for the amino-terminal region
of human prepro alpha 1 [III] collagen.";
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MEDLINE=93293988; PubMed=8514866;
Tromp G., Wu Y., Prockop D.J., Madhatheri S.L., Kleinert C.,
Earley J.J., Zhuang J., Noerrgaard O., Darling R.C., Abbott W.M.,
Cole C.W., Jaakkola P., Rynaenen M., Pearce W.H., Yao J.S.T.,
Majamaa K., Smullens S.N., Gatalica Z., Ferrell R.E., Jimenez S.A.,
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MEDLINE=86187804; PubMed=3754462;
Miskulin M., Dalgleish R., Kluve-Beckerman B., Rennard S.I.,
Tolatsoshev P., Brantly M., Crytal R.G.;
Thuman type III collagen gene expression is coordinately modulated
with the type I collagen genes during fibroblast growth.";
                                                                                  end.";
                                                                                                                                                                                                  a cDNA cloning artefact.";
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                                                                                                                                                                                                                                                               SEQUENCE OF 1065-1466 FROM N.A.
MEDLINE=85087944; PubMed=6096827;
Loidl H.R., Brinker J.M., May M., Pihlajaniemi T., Morrow S.,
[7]
SEQUENCE OF 950-1466 FROM N.A.
MEDLINE=88189827; PubMed=3357782;
Mankoo B.S., Dalgleish R.;
"Human pro alpha 1(III) collagen: cDNA sequence for the 3'
Nucleic Acids Res. 16:2337-2337(1988).
                                                                                                                                                            MEDLINE-89098346; PubMed=3211760;
Molymeux K., Dalgleish R.;
"Human type III collagen 'variant' is a
Nucleic Acids Res. 16:11833-11833(1988).
                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 12:9383-9394(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. 260:4357-4363(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochemistry 25:1408-1413 (1986).
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Gene 78:255-265(1989).
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                                                                                                                                                                                                                                                                                                                                                                      procollagen
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Kontusaari S., Tromp G., Kulvaniemi H., Romanic A.M., Prockop D.J., "A mutation in the gene for type III procollagen (COL3A1) in a family with aortic aneurysms.";
                   mutations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A single base mutation in the gene for type III collagen (COLJA1) converts glycine 847 to glutamic acid in a family with Ehlers-Danlos syndrome type IV. An unaffected family member is mosaic for the mutation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tromp G., Kuivaniemi H., Shikata H., Prockop D.J.; A single base mutation that substitutes serine for glycine 790 of the alpha 1 (III) chain of type III procollagen exposes an arginine and causes Ehlers-Danlos syndrome IV.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H.;
                                                                                                                                                                                                                                                                                                                                                                               VARIANT EDS-IV ARG-828.
MEDLINE=94016385; PubMed=8411057;
Richards A.J., Narcisi P., Lloyd J.C., Ferguson C., Pope F.M.;
"The substitution of glycine 661 by arginine in type III collagen produces mutant molecules with different thermal stabilities and causes Ehlers-Danlos syndrome type IV.";
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MEDLINE=92316511; PubMed=1352273;
Richards A.J., Ward P.N., Narcisi P., Nicholls A.C., Lloyd J.C.,
                                                                                                                           MEDLINE=91045136; PubMed=2235526; Zafarullah K., Kleinert C., Tromp G., Kuivaniemi H., Kontusaari Wu Y., Ganguly A., Prockop D.J.; Wi to A polymorphism in exon 31 of the COL3Al gene."; Nucleic Acids Res. 18:6180-6180(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Characterisation of a glycine to valine substitution at amino position 910 of the triple helical region of type III collagen patient with Ehlers-Danlos syndrome type IV.";
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MEDLINE-91374480; PubMed-1895316;
Richards A.J., Lloyd J.C., Ward P.N., de Paepe A., Narcisi P.,
Jackson C.E., Michels V.V., Kaye M., Kuivaniemi H.; "Sequencing of cDNA from 50 unrelated patients reveals that in the triple-helical domain of type III procollagen are an infrequent cause of acrtic aneuryems.";
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Johnson P.H., Richards A.J., Pope F.M., Hopkinson D.A.;
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                                                        J. Clin. Invest. 91:2539-2545(1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. Chem. 264:1349-1352(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT EDS-IV SER-957.
MEDLINE=89109135; PubMed=2492273;
                                                                                                                                                                                                                                                 VARIANT AORTIC ANEURYSM ARG-786.
MEDLINE=91056145; PubMed=2243125;
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                                                                                                                     VARIANT THR-698.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DNA 7:347-354(1988).
-!- FUNCTION: Collagen type III occurs in most soft connective tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            along with type I collagen.
-!- SUBUNIT: Trimers of identical alpha 1(III) chains. The chains are linked to each other by interchain disulfide bonds. Trimers are also cross-linked via hydroxylysines.
-!- PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94114571; PubMed=8286415; Glumoff V., Maekelae J.K., Vuorio E.; Glumoff V., Maekelae J.K., Vuorio E.; "Cloning of cDNA for rat pro alpha 1(III) collagen mRNA. Different expression patterns of type I and type III collagen and fibronectin genes in experimental granulation tissue."; Biochim. Biophys. Acta 1217:41-48(1994).
                                          0;
    Score 48, DB 1; Length 1466; Pred. No. 0.68; 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 308-482 FROM N.A.
MEDILIE=88296083; PubMed=2456904;
Frankel F.R. Hsu C.-Y.J., Meyers J.C., Lin E., Lyttle C.R.,
Komm B., Mohn K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 73-636 FROM N.A. STRAIN=Sprague-Dawley; TISSUE-Fibroblast; Wurtz T., Elerstroem C., Lundmark C., Christersson C.; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                              13941, 070604;
01-JAN-1990 (Rel. 13, Created)
10-CCT-1994 (Rel. 29, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Collagen alpha 1(III) chain (Fragment).
                                                                                                                                                                                                                  636 AA.
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InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
InterPro; IPR0001861; Fib_collagen_C.
InterPro; IPR001081; Fib_rinogen_C.
InterPro; IPR01007; VWF_C.
Pfam; PF01491; CoLF1; 1.
Pfam; PF01491; Collagen; 6.
ProDom; PD000007; Clg helix; 1.
ProDom; PD002078; Fib_collagen_C; 1.
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EMBL; AJ005395; CAA06510.1; -.
    100.08;
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                                        9; Conservative
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Query Match
Best Local Similarity
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REQUENCE FROM N.A.

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REQUENCE FROM N.A.

REALN=627BL/6; TISSUE=Brain;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.R., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.R., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Mang J., Hsieh F.,

RA Expleton M., Soares M.B., Bonaldo M.F., Caraning L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carning L., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carning D., Prange C.,

RA Brownstein M.J., Wokernan K.J., Mallek J.A., Gunarathe P.H.,

RA Brownstein D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RIJalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

R. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                Gaps
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MEDLINE=95011609; PubMed=7926795;
Toman D., de Crombrugghe B.;
"The mouse type-III procollagen-encoding gene: genomic cloning and complete DNA sequence.";
Gene 147:161-168(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
SMART; SM00038; COLFI; 1.
PROSITE; PS01208; VWFC 1; PARTIAL.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
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0
                                                                               COLLAGEN ALPHA 1(III) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE.
TRIPLE-HELICAL REGION.
NONHELICAL REGION (C-TERMINAL).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                              Score 44; DB 1; Length 636; Pred. No. 1.6; 0; Indels 2; Mismatches
                                                                                                                                                                                                               61A48159F01D01EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                             N -> D (IN REF. 2)
A -> G (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                        CA13 MOUSE STANDARD; PRT; 1464 AA. P08121; Q61429; Q9CRN7; Created) 1-AUG-1988 (Rel. 08, Created) 15-UL-1999 (Rel. 38, Last sequence update) 15-WAR-2004 (Rel. 43, Last annotation update) Collagen alpha 1(III) chain precursor.
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MEDLINE=88167858; PubMed=3443309;
Wood L., Theriault N., Vogeli G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human and mouse cDNA sequences.
                                                                                                                                                                                                               62332 MW;
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Matches 7; Conservative
                                               Collagen, Glycoprotein.
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CHAIN <1 375
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429
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                                                                               Mus musculus (Mouse)
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ID YJHT ECOLI STANDARD; E

AC P39371;

DT 01-FEB-1995 (Rel. 31, Created)

DT 30-MAY-2000 (Rel. 39, Last sequ
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SIGNAL
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                                                                                                                                                                                                                                                               CENTRAINCESTBL/GST. TISSUB-Embaryonic head;

RX MEDLINE-21085660; PubMed-11217851;

RAWAI J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y., Rawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y., Rawai J., Shinagawa A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzawa K., Izawa M., Nishi K., Kiyosawa H., Rondo S., Yamanaka I., RA Alzawa K., Izawa M., Rabiki Y., Robori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., RA Saito T., Matsudi Y., Nikaido I., Pesole G., Quackenbush J., Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Barka J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Annochioni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sazaki H., Sato K., Schoenbach C., Seya T., Shamata Y., Satorch K.-F., Sazaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Anshima Y., Rawaji H., Kohtsuki S., Hayashiawal Y., Rawai Y., Kawaji H., Kohtsuki S., Hayashiawal Y., Rawai Y., Kawaji H., Kohtsuki S., Hayashiawal Y., Rawai Y., Kawaji H., Kohtsuki S., Hayashiawal Y., Rawai Y., Kawaji H., Kohtsuki S., Hayashiawal Y., Landan K., Landan K., Landan K., Landan K., Landan K., Landan K., Kawaji H., Kohtsuki S., Hayashiawal Y., Kawaji H., Kohtsuki S., Hayashiawal Y., Kawaji H., Kohtsuki S., Hayashiawal Y., Landan K., Landan K., Landan K., Landan K., Landan K., Landan K., Landan K., Landan K., Landan K., Kawaji H., Kohtsuki S., Hayashiawal Y., Landan K., Landan K., Landan K., Landan K., Landan K., Landan K., Landan K., Landan K., Landan K., Kawaji H., Kohtsuki S., Hayashiawal Y., Kawaji H., Kohtsuki S., Hayashiawal Y., Landan K., Landan K., Landan K., Landan K., Landan K., Landan K., Landan K., Landan K., Landan K., Landan K., Landan K., Landan K., Landan K., Landan K., Landan K., Landan K., Landan K., Landan K., Kawai K.
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SIMILARITY: Contains 1 VWPC domain.
"Complete nucleotide sequence of the N-terminal domains of the murine alpha-1 type-III collagen chain."; Gene 61:225-230(1987).
                                                                                                              MEDLINE-85131189; PubMed=3972847;
Liau G., Mudryj M., de Crombrugghe B.;
"Identification of the promoter and first exon of the mouse alpha 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDILINE-91274355; PubMed-2054384;
Metsaeranta M., Toman D., de Crombrugghe B., Vuorio E.;
"Specific hybridization probes for mouse type I, II, III and IX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; K03037; -; NOT ANNOTATED CDS.
EMBL; AK019448; BAB3I724.1; -.
EMBL; X57983; CAA41048.1; -.
                                                                                                                                                                                      (III) collagen gene.";
J. Biol. Chem. 260:3773-3777(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1442-1464 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X52046; CAA36279.1; -.
EMBL; BC043089; AAH43089.1; -.
EMBL; BC058724; AAH58724.1; -.
                                                                                                                                                                                                                                                        SEQUENCE OF 810-1464 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M18933; AAA37338.1;
                                                                                                SEQUENCE OF 1-28 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGI:88453; Col3al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A27353; A27353.
PIR; S59856; S59856.
MGD; MGI:88453; Col3a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chains.
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EMBL;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY).
                                                                                                                                                                                                                     Probom; PD000007; Clg_helix; 1.
Probom; PD000078; Flb_collagen_C; 1.
SMART; SM00214; VWC; 1.
SMART; SM00214; VWC; 1.
PROSITE; PS01208; VWFC_2; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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"Analysis of the Escherichia coli genome VI: DNA sequence of region from 92.8 through 100 minutes.";
Nucleic Acids Res. 23:2105-2119(1995).
-i- SIMILARITY: Contains 7 Kelch repeats.
-i- SIMILARITY: STRONG, TO H.INFLUENZAE H10148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O-LINKED (GAL. . .) (BY SIMILARI')
HYDROXYLATION (BY SIMILARITY).
HYDROXYLATION (BY SIMILARITY).
HYDROXYLATION (BY SIMILARITY).
HYDROXYLATION (BY SIMILARITY).
HYDROXYLATION (BY SIMILARITY).
HYDROXYLATION (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NONHELICAL REGION (N-TERMINAL).
TRIPLE-HELICAL REGION.
NONHELICAL REGION (C-TERMINAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 44; DB 1; Length 1464;
Pred. No. 3.7;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL.

AMINO-TERMINAL PROPEPTIDE.

COLLAGEN ALPHA I (III) CHAIN.

CARBOXYL-TERMINAL PROPEPTIDE.

VWPC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRALN=K12 / MOISS;
STRALN=9533456; Pubmed=7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            su-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein yjhT precursor.
YGHT OR B4310.
InterPro; IPR008161; Clg_helix.
InterPro; IPR008160; Collagen.
InterPro; IPR001885; Fib_collagen.
InterPro; IPR001881; Fib_rinogen_C.
InterPro; IPR001001; VWF_C.
Plam; PF01410; Col.FI: 1.
Pfam; PF01410; Col.FI: 1.
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HS21 MAIZE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P24631;
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                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                 EcoGene, EG12562, Anilon, Anilon, EcoGene, EG12562, Kelch rep.

InterPro, IPR006652, Kelch rep.

Pfam, PF01344, Kelch; 2.

Pyorhetical protein; Kelch repeat; Repeat; Signal; Complete proteome. SIGNAL

1 POTENTIAL.

CHAIN 20 369 HYPOTHETICAL PROTEIN YJHT.

REPEAT 40 48 KELCH 1.

REPEAT 86 137 KELCH 2.
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                   01-OCT-1989 (Rel. 12, Created)
10-OCT-1989 (Rel. 12, Last sequence update)
11-OMA-2004 (Rel. 43, Last annotation update)
Keratin, type II cytoskeletal 3 (Cytokeratin 3) (K3) (CK3) (65 kDa cytokeratin).
                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=87254239; PubMed=2439698;
Klinge E.M., Sylvestre Y.R., Freedberg I.M., Blumenberg M.;
"Evolution of keratin genes: different protein domains evolve by
                                                                                                                                                                               ;
                                                                                                                                                             Score 36; DB 1; Length 368;
Pred. No. 28;
0; Mismatches 1; Indels
                                                                                                                                             39572 MW; 1194F392C51EA204 CRC64;
                                                                                                                                                                                                                                                      629 AA.
entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                      KELCH 1.
KELCH 2.
KELCH 3.
KELCH 4.
KELCH 5.
KELCH 6.
                    EMBL; U14003; AAA97206.1; ALT INIT.
EMBL; AE000501; AAC77266.1; ALT_INIT.
                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                  J. Mol. Evol. 24:319-329(1987).
                                                                                                                                                            75.0%;
87.5%;
                                                                                                                                                    Query Match
Best Local Similarity 8/...
7; Conservative
                                                                                                                                                                                                                                                     STANDARD;
                                                                       19
368
84
1137
1173
2219
2265
336
                                                                                                                                                                                                           341 İĞĞETAĞĞ 348
                                                                                                                                                                                                                                                                                                                                                                                          different pathways.";
                                                                                                                                                                                            1 IGGEKAGG 8
                                                                                                                                             368 AA;
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                    K2C3 HUMAN
                                                                                                                                             SEQUENCE
                                                                                                     REPEAT
REPEAT
                                                                                                                             REPEAT
REPEAT
                                                                                                                                                                                                                                                           P12035;
                                                                                                                     REPEAT
                                                                                                                                                                                                                                    RESULT 5
K2C3_HUMAN
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0
-!- MISCELLANEOUS: There are two types of cytoskeletal and microfibrillar keratin: I (acidic, 40-55 kDa) [K9 to K20] and II (neutral to basic, 56-70 kDa) [K1 to K8].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 122100; -.
GO; GO:0005882; C:intermediate filament; NAS.
GO; GO:00051882; F:structural molecule activity; NAS.
GO; GO:0007010; P:cytoskeleton organization and biogenesis; NAS.
InterPro; IPR001664; IF.
InterPro; IPR002957; Keratin I.
InterPro; IPR003054; Keratin II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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Intermediate filament; Coiled coil; Keratin; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COIL 2. PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.0%; Score 36; DB 1; Length 629; 75.0%; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2E748619A828BCD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E -> K (in MCD).
/FTId=VAR 003868.
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01-JUN-1994 (Rel. 29, Last annotation update)
17.5 kDa class II heat shock protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COIL 1A.
LINKER 1.
COIL 1B.
                                                                                                                                                                                                                                                                                                                                             EMBL; X05418; CAA28991.1; -.. EMBL; X05419; CAA28992.1; ALT SEQ. EMBL; X05420; CAA28993.1; ALT—SEQ. EMBL; X05420; CAA28993.1; ALT—SEQ. EMBL; X05420; CAA28995.1; ALT—SEQ. EMBL; X05421; CAA28995.1; ALT—SEQ. GENEW; HONC: 6440; KRT3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam, PF00038, filament, 1.
PRINTS, PR01248, TYPEIKERATIN.
PRINTS, PR01276, TYPEZKERATIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 75.0 hes 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 GGSRAGGF 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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198
234
255
347
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                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-98037514; PubMed=9371463;

Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,

Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

Aldredge T., Bashirzadeh P., Lumm W., Pothier B., Qiu D.,

A padafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,

Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,

McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

A mcDougall S., Shimer G. Methanobacterium thermoautotrophicum

"Complete genome sequence of Methanobacterium thermoautotrophicum

"Complete genome sequence of Methanobacterium thermoautotrophicum

"Complete genome sequence of Methanobacterium thermoautotrophicum

"Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;

"Bacteriol. 179:7135-7155 (1997).

"Bacteriol. 179:7135-7155 (1997).

"ENWINTANOFURAN (CHO-MER). CAN ONLY

OXIDISE FORMYLMETHANOFURAN THIS ENZYME IS OXYGEN-LABILE.

"CATALITY CATILYTY: FORMYLMETHANOFURAN H H (2)O + acceptor = CO(2)

+ methanofuran + reduced acceptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
SIMILARITY: PLANTS HAVE FOUR CLASSES OF HSP20: CLASS I AND II WHICH ARE CYTOPLASMIC; CLASS III WHICH IS IN THE CHLOROPLAST AND CLASS IV WHICH IS IN THE ENDOMEMBRANE. THIS PROTEIN BELONGS TO CLASS II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tungsten-containing formylmethanofuran dehydrogenase II subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
0
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Archaea, Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae, Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.9%; Score 35; DB 1; Length 161; 85.7%; Pred. No. 19; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17511 MW; 3E60A8DD4396577C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002068; Hsp20.
InterPro; IPR008978; HSP20_chap.
Pfam; PF00011; HSP20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01031; HSP20; 1.
Heat shock; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X54076; CAA38013.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity Bs...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S14998; S14998.
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GGDKAGG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGEKAGG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EC_1.2.99.5).
FWDC OR MTH1558.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Delta H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MaizeDB; 51309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FWDC METTH
                                                                                                                                               family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FWDC_METTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- COFACTOR: Tungsten.
-!- PATHWAY: Methanogenesis; first step.
-!- SUBUNIT: THIS ENZYME IS COMPOSED OF SEVEN SUBUNITS FWDF (65 kDa),
-!- SUBUNIT: THIS ENZYME (31 kDa), FWDD (15 kDa), FWDE, FWDF, AND FWDG
                  -!- PATHWAY: Methanogenesis; first step.
-!- SUBUNIT: THIS ENZYME IS COMPOSED OF SEVEN SUBUNITS FWDA (65 kDa),
FWDB (53 kDa), FWDC (31 kDa), FWDD (15 kDa), FWDE, FWDF, AND FWDG-
-!- INDUCTION: By growth on tungsten or molybdenum under anaerobic conditions.
-!- SIMILARITY: Belongs to the fwdC/fmdC family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: Formylmethanofuran + H(2)O + acceptor = CO(2) + methanofuran + reduced acceptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-96163477; PubMed-8575452;
Hochheimer A., Schmitz R.A., Thauer R.K., Hedderich R.;
Hochheimer A., Schmitz R.A., Thauer R.K., Hedderich R.;
Hochheimer A., Schmitz R.A., Thauer R.K., Hedderich R.;
The tungsten formylmethanofuran dehydrogenase from Methanobacterium rehermoautotrophicum contains sequence motifs characteristic for enzymes containing molybdopterin dinucleotide.";

Bur. J. Biochem. 234:910-920(1995).
I- FUNCTION: CATALYZES THE REVERSIBLE OXIDATION OF CO(2) AND METHANOFURAN (MFR) TO N-FORNYLMETHANOFURAN (CHO-MFR). CAN ONLY OXIDISE FORMYLMETHANOFURAN. THIS ENZYME IS OXYGEN-LABILE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome. [GW]-X-X-M-X-X-G-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FWDC_METTM STANDARD; PRT; 270 AA.

OS9579; 008493;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Tungsten-containing formylmethanofuran dehydrogenase II subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      043A9FFBBA554D36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oxidoreductase; Tungsten; Methanogenesis; Repeat; DOMAIN 80 213 7 X 13 AA REPEATS OF X-[IL]-X-[IV]-X-G.
REGULATION: Not inactivated by cyanide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 32;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.9%; Score 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000916; AAB86032.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28641 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; H69074; H69074.
InterPro; IPR002489; DUF14.
Pfam; PF01493; GXGXG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92
1111
130
156
175
194
213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            270 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IGGEKAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=79929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EC 1.2.99.5).
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9
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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CDNAs."
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                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A MEDLINE=2184891; PubMed=11859360;

W MEDLINE=2184891; PubMed=11859360;

Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Squorco J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Erown S., Chillingworth T., Churcher C.M., A Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A. Genlles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., RA Moncey P., Moule B., Howarth S., Huckle E.J., Hunt S., Jagels K., A James K., Jones M., Leather S., McDonald S., McLean J., RA Mooney P., Moule S., Muragal, K., Murphy L., Niblett D., Odell C., RA Mooney P., Moule S., Muragal, K., Murphy L., Niblett D., Odell C., RA Retter K., O'Neil S., Parsson D., Quail M.A., Rabbinowitsch E., RA Squares R., Squares R., Stevens K., Sakelton J., Simmonds M., Squares R., Squares S., Stevens K., RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., RB Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., RB Ger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Reger P., Zimmermann W., Wedler H., Wambutt R., Purnelle S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative NADPH dehydrogenase C5H10.04 (EC 1.6.99.1) (Old yellow enzyme
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                              EMBL; X0970; CAA6121....

EMBL; X07970; CAA612489; DUF.4.

Pfam; PF01493; GXGXG; 1.

Oxidoreductase; Tungsten; Methanogenesis; Repeat.

80 213 7 X 13 AA REPEATS OF [GW]-X-X-M-X-X-G-X-IIJ]-X-[IV]-X-G.
-!- INDUCTION: By growth on tungsten or molybdenum under anaerobic
                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 1; Length 270; Pred. No. 32; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                               28554 MW; E0A369D2ACFEC46F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae,
             conditions.
-!- SIMILARITY: Belongs to the fwdC/fmdC family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       382 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                       72.9%;
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.v.,
Accountative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                           :||| |||
200 VGGEMAGG 207
                                                                                                                                                                                                                                                                           144
163
182
182
201
270 AA;
                                                                                                                                                                                                                                                                                                                                                                                                          1 IGGEKAGG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPACSHIO.04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OYEA SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=972;
                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                  REPEAT
REPEAT
REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
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          Moore K., Hurst S.M.,
a V.A., Garzon A., Thode G.,
Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                         -i- CATALYTIC ACTIVITY: NADPH + acceptor = NADP(+) + reduced acceptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -I- FUNCTION: This is a receptor for interleukin-9.
-!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.
-!- SIMILARITY: Belongs to the type I cytokine family of receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Renauld J.C., Druez C., Kermouni A., Houssiau F., Uyttenhove C., van Roost E., van Snick J., "Expression cloning of the murine and human interleukin 9 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BMBL; Z49811; CAA89954.1; -.
PIR; S55482; S55482.
HSSP; 002899; 10YC.
GeneDB SPombe; SPAC5H10.04; -.
InterPro; IPR001155; Oxidored FMN.
Pfam; PF00724; oxidored FMN.
Hypothetical protein; Oxidoreductase; NADP; Flavoprotein; FMN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Subfamily 4.
                                                                                                                                                                                                                                                                                                                                                 -1- SUBUNIT: Homodimer or heterodimer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43813 MW; 3F7939599CA167D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 89:5690-5694(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.9%; Score 35; DB 1; 85.7%; Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Interleukin-9 receptor precursor (IL-9R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           468 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 GEKSGGF 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 GEKAGGF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=T-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IL9R MOUSE
Q01114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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InterPro; IPR001969; Aspprotease_AS
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                                                                                                                                                                      NP BIND
DISULFID
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                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                              RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nikiforov V., Yurieva O., Kholodii G., Minakhin L., Gorlenko Z., Kalyavava E., Mindlin S.;
Kalyavava E., Mindlin S.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Resistance to Hg(2+) in bacteria appears to be governed by a specialized system which includes mercuric reductase. Meraprotein is responsible for volatilizing mercury as Hg(0).
-!- CATALYTIC ACTIVITY: Hg + NADP(+) + H(+) = Hg(2+) + NADPH.
-!- CATALYTIC ACTIVITY: Hg + NADP(+) + H(+) = Hg(2+) + NADPH.
-!- COFACTOR: Binds I FAD per subunit (By similarity).
-!- SIMINITY: Helongs to class is a redox-active disulfide bond.
-!- SIMILARITY: Belongs to class I pyridine nucleotide-disulfide
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
BBE71179FD72E29A5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Alcaligenes.
                                                                                                                                                                                                                                Score 35; DB 1; Length 468;
Pred. No. 54;
                                                                                                                                                                                                                                                        1; Indels
                                                                                                                       INTERLEUKIN-9 RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                             MGD; MGI:966564; II9r.
InterPro; IPR002996; CRIA.
InterPro; IPR008957; FW III-like.
InterPro; IPR00851; Hentopoptn S F1.
PROSITE; PS01355; HEMATOPO REC F7; 1.
Receptor; Transmembrane; Glycoprotein; Signal; T-cell.
                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Mercuric reductase (EC 1.16.1.1) (Hg(II) reductase).
                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -! - SIMILARITY: Contains 1 HMA domain.
    send an email to license@isb-sib.ch)
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InterPro; IPR006121; HeavyMe_transpt.
InterPro; IPR000815; Hg_reductase.
InterPro; IPR006191; Metal_bind.
                                                                                                                                                                                                            52260 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Y08993; CAA70190.1; -. HSSP; Q04656; 1AW0.
                                                                                                                                                                                                                                  72.9%;
                           EMBL; M84746; AAA37871.1; -.
                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Alcaligenes sp.
Plasmid IncHI2 pMER610.
                                                                                                                                468
2270
2291
242
1116
155
                                                                                                                                                                                                                                                                                                      GGOKAGAF 53
                                                                                                                                                                                                                                                                                GGEKAGGF 9
                                                                                                                                                     271
292
149
116
155
468 AA;
                                                                                                                                                                                                                                             Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=512;
                                                                                                                                                                                                                                                                                                                                                             MERA ALCSP
P94188;
                                                                                                                                CHAIN
DOMAIN
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                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                    Query Match
                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                    MERA_ALCSP
                                                                                                                                                                                                                                                  Best Loc
Matches
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-1- CAJALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
28-REB-2003 (Rel. 41, Last annotation update)
POL polyprotein [Conteains: Protease (Retropepsin) (BC 3.4.23.-);
Reverse transcriptase (EC 2.7.7.49); Ribonuclease H (EC 3.1.26.4)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- PTW: Cleavage sites that yield the mature proteins remain to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- MISCELLANDUS: THIS IS AN AFRICAN MANDRILL ISOLATE.
-!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A2; ALSO
KNOWN AS THE RETROPEPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                            Prami Provisi Harry .

Prami Provisi Harry .

Prami Provisi Provisi Pradox dim; 1.

PRINTS; PRO0945; FADPUN.

PRINTS; PRO0945; FADPUN.

PRINTS; PRO0913; FADPUN.

PROSTIE; PS000139; FAD_DYL_redox; 1.

PROSTIE; PS00076; PRINTDINE_REDOX 1; 1.

PROSTIE; PS00076; PRINTDINE_REDOX 1; 1.

PROSTIE; PS00076; PRINTDINE_REDOX 1; 1.

PROSTIE; PS00076; PRINTDINE_REDOX 1; 1.

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PROSTIE; PS00076; PRINTDINE_REDOX 1; 1.

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PROSTIE; PS00076; PRINTDINE_REDOX 1; 1.

PROSTIE; PS00076; PRINTDINE_REDOX 1; 1.

PROSTIE; PS00076; PRINTDINE_REDOX 1; 1.

PROSTIE; PS00076; PRINTDINE_REDOX 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 FAD (ADP PART) (BY SIMILARITY). REDOX-ACTIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.9%; Score 35; DB 1; Length 559; 85.7%; Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0603DDD6B13CB519 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simian immunodeficiency virus (isolate GBI).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MERCURY (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1009 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
InterPro; IPR001100; Pyr_redox.
InterPro; IPR004099; pyr_redox_dim.
                                                                                                                                                                                                                                                                                                                                                                                                               HMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58019 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M27470; AAB49569.1; -.
HSSP; P03366; 1HRH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match (2.7%;)
Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                         Pfam; PF00403; HMA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                           126
134
134
556
557
557
559 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
60S ribosomal protein L12.
(RPL12A OR SPCC31H12.04C) AND (RPL12B OR SPCC16C4.13C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (RPL12A AND RPL12B).
                       InterPro; IPR003308; Integrase_Zn. InterPro; IPR009007; Pept_A_acid. InterPro; IPR001995; Peptidase_A2. InterPro; IPR002156; RNaseH. InterPro; IPR001584; Rve. InterPro; IPR000477; RVTse.
                                                                                                                                                                                                                                               Pfam; PF00552; integrase; 1.
Pfam; PF02022; Integrase_Zn; 1.
Pfam; PF00075; rnaseH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 GGEERGGF 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 GGEKAGGF 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RL12 SCHPO
075000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
RL12_SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ES2;
MEDLINE=90568592; PubMed=1975583;
MEDLINE=90568592; PubMed=1975583;
Behrmann I., Hillemann D., Puehler A., Strauch E., Wohlleben W.;
"Overexpression of a Streptomyces viridochromogenes gene (glnII)
encoding a glutamine synthetase similar to those of eucaryotes confers resistance against the antibiotic phosphinothricyl-alanyl-alanine.";
J. Bacteriol. 172:5326-5334(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
FUNCTION: This protein binds directly to 26S ribosomal RNA (By
                similarity).
-!- MISCELLANEOUS: There are two genes for L12 in S.pombe.
-!- SIMILARITY: Belongs to the L11P family of riboscomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces viridochromogenes.

Bacteria, Actinobacteria, Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.

NCBI_TaxID=1938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.8%; Score 34; DB 1; Length 165; 75.0%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM06649; RLJ1; 1.
PROSITE; PS00359; RIBOSOMAL LL1; 1.
RIBOSOMAL protein; RNA-binding; Multigene family.
SEQUENCE 165 AA; 17666 MW; FC777B46CD08F005 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 protein.
240 AA; 23914 MW; 09DB6BEE681F7E2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical 23.9 kba protein in glnII region (ORF2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.8%; Score 34; DB 1;
85.7%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                              HSSP, P29395; IMMS.
GeneDB SPombe; SPCC16C4.13c; -CenseDB SPombe; SPCC131HLZ.04c; -CenseDB SPOMDe; SPC031HLZ.04c; -CenseDB SP003011; Ribosomal_L11; Pfam; PF00299; Ribosomal_L11; -CenseDE SP03946; Ribosomal_L11; -CenseDE SP03946; Ribosomal_L11, N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                        EMBL; AL031824; CAA21221.1; -.
EMBL; AL031535; CAA20752.1; -.
PIR; T41103; T41103.
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Hypothetical protein.
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Best Local Similarity
Matches 6; Conserv
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MEDLINE=95050819; PubMed=7961958;
MEDLINE=95050819; PubMed=7961958;
MEDLINE=95050819; PubMed=7961958;
MEDLINE=95050819; PubMed=7961958;
Nan B., Yang D., Brady M., Parkinson A.;
Incalization, and relationship to rat liver hydrolase.";
J. Biol. Chem. 269:29688-29696(1994).
Incalization: NNOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN THE DETOXIFICATION OF ESTER AND ALPHA-NAPHTHYL ACETATE: IT ALSO
NITROPHENYL ACETATE AND ALPHA-NAPHTHYL ACETATE: IT ALSO
HYDROLYZES ACETANILIDE AND, DISTINCTIVELY, PALMITOYL-COA.
INCALLY A CAPLAYILY A CARDONYLIC ESTER + H(2)O = an alcohol + a
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064573; 062679;
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Liver carboxylesterase 4 precursor (EC 3.1.1.1) (Carboxyesterase ES-4)
(Microsomal palmitoyl-CoA hydrolase) (Kidney microsomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
      Gaps
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SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
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PROSITE; PS00122; CARBOXYLESTERASE B 1; 1.
PROSITE; PS00941; CARBOXYLESTERASE B 2; 1.
Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum; Signal; Multigene family.
BY SIMILARITY.
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STRAIN=Sprague-Dawley; TISSUE=Liver;

MEDLINE=Sprague-Dawley; TISSUE=Liver;

MEDLINE=Sed190723; PubMed=8611161;

Robbi M., van Schaftingen E., Beaufay H.;

Robbi M., van Schaftingen E., Beaufay H.;

Richoning and sequencing of rat liver carboxylesterase ES-4

(microscomal palmitoyl-CoA hydrolase).";
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LIVER CARBOXYLESTERASE 4.
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      Mismatches
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EMBL; U10697; AAA64638.1; -.
PIR; 862788; 852788.
HSSP; P21836; 1MAA.
InterPro; IPR002018; CarbesteraseB.
InterPro; IPR003086; R target_S.
InterPro; IPR0030379; Ser_estrs.
Pfam; PP00135; COesterase; 1.
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Pred. No. 98;
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM protein - protein search, using sw model	Run on: September 18, 2004, 04:00:08; Search time 31.9412 Seconds (without alignments) 88.903 Million cell updates/sec	Title: US-10-615-959-41 Perfect score: 48 Sequence: 1 IGGEKAGGF 9	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 1017041 seqs, 315518202 residues	Total number of hits satisfying chosen parameters: 1017041	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries	*:* le	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Result Query No. Score Match Length DB ID Description	1 48 100.0 1163 4 Q8N6U4 2 44 91.7 338 11 Q8BJU6 Q8BK73 mus musculu Q8BK73 mus musculu Q8BK73 mus musculu Q8BK73 mus musculu Q8BK73 mus musculu Q8BK73 mus musculu Q8BK74 11 Q8BLW4 Q8TGUL Q8TG

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DT 01-CCT-2002 (TrEMBLrel. 22, Last sequence update)

T 01-CCT-2003 (TrEMBLrel. 25, Last annotation update)

DT 01-CCT-2003 (TrEMBLrel. 25, Last annotation update)

DE 1V, autosomal dominant.)

E 1V, autosomal dominant.)

C ENKARYOTA: Metazoa; Cype III, alpha 1 (Ehlers-Danlos syndrome type in annotation update)

E 1V, autosomal dominant.)

C ENKARYOTA: Metazoa; Cype III, alpha 1 (Ehlers-Danlos syndrome type in annotation update)

C Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

C Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

C Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

E SUBMICTEG (APR-2002) to the EMBL/GenBank/DDBJ databases.)

R STARUBEYS

C CO:0005201; F:extracellular matrix structural constituent; IEA.

DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

BR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

BR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

BR InterPro; IPRO01085; Fib collagen. C.

BR InterPro; IPRO01085; Fib collagen. C.

BR Pfam; PFO1191; COLLEG: 1.

BR PFOND; PFO039; COLFF: 1.

BR SMART; SM00214; WWC: 1.

C SEQUENCE 1163 AA; 111899 MM; 9EOCGEBIE94D6357 CRC64;

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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Buthaia, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
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SC STRAIN=CS7BL/6J; TISSUE=Head;

SC MEDLINE=22354683; DubMed=12466851;

RATINE=22354683; DubMed=12466851;

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RA The RIKEN Genome Exploration Research Group Phase I & II Team;

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 44;
2; Mismatches 0; Indels 0
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InterPro; IPR000885; Fib_collagen_C.
Pfam; PF01410; COLFI; 1.
Pfam; PF01391; COLFI; 1. 16.
ProDom; PD000007; Clg helix; 1.
ProDom; PD000007; Clg helix; 1.
SMART; SM00038; COLFI; 1.
SMART; SM00038; COLFI; 1.
SMART; SM00038; COLFI; 1.
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SMART; SM00038; COLFI; 1.
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SMART; SM00038; COLFI; 1.
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SMART; SM00214; VWC; 1.
PROSITE; PS01208; VWFC_1; 1.
SEQUENCE 1464 AA; 138947 M
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity 77.00
7, Conservative
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964 VGGEKSGGF 972
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Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Gones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                91.7%; Score 44; DB 11; Length 1464; 77.8%; Pred. No. 53; tive 2; Mismatches 0; Indels (
                                                                                                                                                                                        Strausberg R.; Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC052399; AAH52398.1; ... Hypothetical protein. SEQUENCE a1464 AA; 138971 MW; 2B38BC27AF21590B CRC64;
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                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
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GCVT OR R01549 OR SMC02047.
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InterPro; IPR006222; GCV T.
Pfam; PF01571; GCV_T; 1.
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Best Local Similarity 87.50,
-has 7; Conservative
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les 7; Conservative
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1206 VGGEKSGGF 1214
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C57BL/6; TISSUE=Brain;

M Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Aleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Marmann R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RAchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nullalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                           STRAIN-C57BL/64; TISSUB=Aorta, and Vein;
MEDLINE-22354683; PubMed=12466851;
The FANTOM Consortium,
The FANTOM Consortium,
The RATION Genome Exploration Research Group Phase I & II Team;
Analyais of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:653-573(2002).
MGD; MGI:88453; Collagen; I.A.
MGD; MGI:88453; Collagen; IEA.
GO; GO:0005581; C:collagen; IEA.
GO; GO:0005581; F:extracellular matrix structural constituent; IEA.
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                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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InterPro; IPR008161; Clg helix.
InterPro; IPR001801; Collagen.
InterPro; IPR001801; Fibrinogen.C.
InterPro; IPR001801; WPF.C.
Pfam; PF01410; CoLF!; 1.
Pfam; PF01410; CoLF!; 1.
Pfam; PF01391; Collagen; 18.
ProDom; PD000007; Clg_helix; 1.
ProDom; PD000078; Fib_collagen_C; 1.
SWART; SW000218; Fib_collagen_C; 1.
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 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
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01-MAR-2003 (TrEMBLrel.
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Mus musculus (Mouse).
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                                             Collagen alpha 1.
                                                                                                                   NCBI_TaxID=10090;
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                                                                         Mus musculus
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Ambiline=11396507; PubMed=11481430;

Acapela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,

Babistard P., Becker A., Boutry M., Cadieu B., Dreano S., Gloux S.,

Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,

A Pohl T., Portetelle D., Puhler A., Purnelle B., Ramsperger U.,

Analysis of the chromosome sequence of the legume symbiont

T. Analysis of the chromosome sequence of the legume symbiont

Sinorhizobium meliloti strain 1021 ".

Broc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).

R EMBL, ALS91787, CAc46128.1;

R GO: GO:0004374; F:gliycine cleavage system; IEA.

GO: GO:0006440; F:transferase activity; IEA.

GO: GO:0006546; P:glycine catabolism; IEA.
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                  032009,
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Probable aminomethyltransferase (Glycine cleavage system T protein)
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85.4%; Score 41; DB 16; Length 379; 87.5%; Pred. No. 43; tive 1; Mismatches 0; Indels
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SEQUENCE 379 AA; 40369 MW; 047C7002EF5A30CF CRC64;
379 AA.
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39 GGEKAĞĞ 45

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8

2 GGEKAGG

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99 GGEAAGGF 106
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                                                                                                                                                                                                                                                                                   NCBI_TaxID=56636;
                                                                                                                                                                                                                                   Aeropyrum pernix.
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Q8S1V9
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                                                               RESULT 10
                                                                                 Q9YFP0
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                                                                                                                                                                                                                                             STRAIN-GOEL (7 ATCC BAR-199 / DSM 3647 / OCM 88;

MEDLINE-22120827; Pubbled=12125824;

Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,

Martinez-Arias R., Henne A., Wiezer A., Baeumer S., Jacobi C.,

Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,

Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,

Fritz H.-J., Gottschalk G.,

Fritz H.-J., Gottschalk G.,

The genome of Merhanosarcina mazei: evidence for lateral gene

transfer between Bacteria and Archaea.";

J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
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Archaea; Buryarchaeota, Buryarchaeota orders incertae sedis;
Methanosarcinales; Methanosarcinaceae; Methanosarcina.
NCBI_TaxID=2209;
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Pred. No. 96;
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Conserved protein.
                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Glycine cleavage system protein T2.
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                                   372 AA
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                                 PRT;
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Best Local Similarity 66.,
6; Conservative
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                                     PRELIMINARY;
                                                                                                                                                                        Vibrio parahaemolyticus
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                                       087101
RESULT 8
Q87101
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group).
Bukaryota, Viitdiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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R GO; GO:0016020; C. membrane; IEA.

R GO; GO:0004222; F. metalloendopeptidase activity; IEA.

R GO; GO:0004202; F. metalloendopeptidase activity; IEA.

R GO; GO:0006208; F. proteclysis and peptidolysis; IEA.

R GO; GO:0006508; P: proteclysis and peptidolysis; IEA.

R InterPro; IPR001193; Pept M50 SREBP.

R InterPro; IPR0060193; Pept M50 SREBP.

R InterPro; IPR0060193; Pept M50 SREBP.

R Pfam; PF00595; Pept M50 SREBP.

R Pfam; PF00595; Pept M50 SREBP.

R Pfam; PF00595; Pept M50 SREBP.

R Pfam; PF00595; Pept M50 SREBP.

R PRIMTS; RR01000; SREBPSZPTASE.

R SMART; SM00228; PDZ; 1.
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                                                                                                                                                                                                                   Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protease; Metalloprotease; Complete proteome.
SEQUENCE 383 AA; 39729 MW; FE7289C4F06E8F76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative beta-amylase.
                                                                             Last sequence update)
Last annotation update)
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Peet Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 1;
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                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence up
01-OCT-2003 (TrEMBLrel. 25, Last annotation
383AA long hypothetical S2P metalloprotease
383 AA
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  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99310339; PubMed=10382966;
                                                                                                                                                                                                                                                                  Desulfurococcaceae; Aeropyrum
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     PRELIMINARY;
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RY SEQUENCE FROM N.A.

RA MEDINES-1590369, PubMed=11733140;

RA Martinez-Mir A., Canestro C., Gonzalez-Duarte R., Albalat R.;

RT "Characterization of the amphioxus presentlin gene in a high gene-
RT density genomic region illustrates duplication during the vertebrate cansity genomic region illustrates duplication during the vertebrate lineage.";

RL Gene 279:157-164(2001).

RR MEDI, AR369801, AAL40416.1;

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.

RO; GO:0003700; F:transcription of transcription, DNA-dependent; IEA.

RO; GO:000447; HTH LysR.

DR HIGFPC; IPRO0108; Peptidase A22.

RICEPPC; IPRO0108; Persemilin; 1.

DR PRINTS; RR01072; PRESEMILIN.

DR PROSITE; PS00044; HTH LYSR FAMILY; 1.

ROSITE; PS00044; HTH LYSR FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=21590369; PubMed=11733140;
MAILINE=21590369; PubMed=11733140;
MAILINE=21590369; PubMed=11733140;
MAILINE=21590369; PubMed=11733140;
Characterization of the amphioxus presenting ene in a high genedensity genomic region illustrates duplication during the vertebrate Gene 279:157-164(2001).
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EMBL; AF36990; AAL40414.1; -.

EMBL; AF36990; AAL40414.1; JOINED.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0003700; F:transcription factor activity; IEA.

GO; GO:000742; P:intracellular signaling cascade; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR000647; HTH LysR.

InterPro; IPR001087; Peptidase A22.

InterPro; IPR01108; Peptidase A22.

FRINTS; PR01072; PRESENILIN.

SMART; SM00730; PSN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Branchiostoma floridae (Florida lancelet) (Amphioxus).
Eukaryota, Metazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                                                                                                                                                                                                                                                                                                                                                       ;
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SEQUENCE 525 AA; 57598 MW; 2814CF77A80F07DE CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Presentilin.
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fatches 6; Conservative
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Matches 6; Conserv
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Bukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
Branchiostoma
NCBI_TaxID=7739;
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Pseudomonadaceae; Pseudomonas.
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                            STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=FALL,
He J., Rahme L.G.;
He J., Rahme L.G.;
"Pseudomonas aeruginosa PA14 pathogenicity island (PAPI) 1.";
"Pseudomonas aeruginosa PA14 pathogenicity databases.
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY273869; AAP84143.1; -.
Hypothetical protein.
SEQUENCE 460 AA; 48289 MW; A56P37B515F2F2BD CRC64;
                                                                                                                                                                                                                                                                                            79.2%; Score 38; DB 10; Length 415; 100.0%; Pred. No. 1.6a+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 79.2%; Score 38; DB 2; Length 460; Similarity 75.0%; Pred. No. 1.8e+02; 6; Conservative 2; Mismatches 0; Indels
                                                                         clone:POS03C12.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003268; BAB89698.1; -.
                                                                                                                                01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    460 AA
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Best Local Similarity 100.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa.
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SEQUENCE FROM N.A.
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                                                                                                                          Gramene;
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                       01-0CT-2003 (TrEMBLrel. 25, Created)
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0SJNBA0053K19.24.
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

September 18, 2004, 03:47:39; Search time 58.8824 Seconds (without alignments) 52.784 Million cell updates/sec Run on:

US-10-615-959-42 56 1 IAGIGGEKAGG 11 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: geneseqp1980s:\*
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ABB09628 AAE02534 AAE02533 AAR92068	AAB61740 AAB61741 AAY68425 AAY68436	AAB51275 ABG08457 AAG16397 AAY29227	AAW23083 ABB92411 AAY29125 ABU34804 ADB80237 ABG25363
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#### ALIGNMENTS

Type II collagen; immunoassay; cartilage; telopeptide; human; type III collagen. Human type III collagen carboxy-telopeptide fragment. AAB61742 standard; peptide; 11 AA. 99US-00335098. 99US-0141574P. 99US-0142274P. 99US-0142675P. 99WO-US029357. (WASH-) WASHINGTON RES FOUND. (first entry) WO200079284-A1. Synthetic. Homo sapiens. 10-DEC-1999; 20-APR-2001 17-JUN-1999; 28-DEC-2000 02-JUL-1999; 07-JUL-1999 30-AUG-1999; AAB61742; RESULT 1 AAB61742 

Eyre DR;

WPI; 2001-146859/15.

Assay for detecting cross-linked telopeptide analytes indicative of type II collagen resorption in vivo in a body fluid sample, comprises contacting the sample with an antibody which binds to the analyte.

Disclosure, Page 15; 34pp; English.

The invention relates to immunoassays for measuring type II collagen (cartilage) resorption in vivo. The method of analysing a body fluid sample for the presence of an analyte indicative of a physiological condition, involves contacting the body fluid sample with an antibody (Ab) which binds to the analyte, detecting binding of Ab in the body fluid sample, and correlating any detected binding to the physiological condition. The analysis is useful for measuring type II collagen (cartilage) resorption in vivo, for distinguishing between resorption of

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assay for detecting cross-linked telopeptide analytes indicative of type II collagen resorption in vivo in a body fluid sample, comprises contacting the sample with an antibody which binds to the analyte.
  non-mineralized and mineralized cartilage, and for measuring total cartilage resorption in vivo. The present sequence represents a linear synthetic peptide based on the carboxy-terminal telopeptide sequence of
                                                                                                       Gaps
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                                                                                100.0%; Score 56; DB 4; Length 11; 100.0%; Pred. No. 0.016;
                                                                                                       0; Indels
                                                                                                                                                                                                                                                                      Human type III collagen carboxy-telopeptide fragment.
                                                                                                         0; Mismatches
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                                                                                                                                                                                                           AAB61743 standard; peptide; 12 AA.
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99US-0141574P.
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                                                                                                                                                                                                                                                      (first entry)
                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
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                                         human collagen type III
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                                                               Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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Query Match Best Local Similarity

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The invention relates to a method of determining the rate of biosynthesis or breakdown of at least one inaccessible biological molecule in a confice the method is useful for diagnosis or monitoring and treatment subject. The method is useful for diagnosis or monitoring and treatment of diseases associated with an altered rate of biosynthesis/breakdown of of diseases associated with an altered rate of biosynthesis/breakdown of confice allowed the subject of the second treatment of the second treatment of the second treatment of the second treatment of diseases allowed the method is callowed; muscular dystrophy; athletic diabetes mellitus; muscle-wasting syndromes; muscular dystrophy; athletic constraining and cancer. The method is also useful for screening candidate training and cancer. The method is also useful for screening candidate creating mechanism studies and determining the risk of developing the dirugs, drug mechanism studies and determining the risk of developing the disease. The present sequence is human C-terminal telopeptide alpha 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Determining rate of biosynthesis or breakdown of inaccessible biological molecules, useful e.g. for diagnosis or monitoring treatment, by administering labeled precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, therapy; osteoporosis, left-ventricular hypertrophy; scleroderma; liver cirrhosis; congestive heart failure; multiple sclerosis; fibrosis; coal-miner's pneumoconiosis; muscle-wasting syndrome; diabetes mellitus; rheumatoid arthritis; Alzheimer's disease; muscular dystrophy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                               Human C-terminal telopeptide alpha 1 #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 24; Page 99; 105pp; English.
                                                                                                                                                                                                                               AAE38632 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-FEB-2002; 2002US-0356008P.
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Best Local Similarity 1000.
Loca 11; Conservative
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1 IAGIGGEKAGG 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                telopeptide alpha
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                                                                                                                                                                                                                                                                                                                   AAE38632;
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Alcoholic cirrhosis; biliary cirrhosis; hepatitis; schistosomiasis; cardiac fibrosis; Crohn's disease; diabetic nephropathy; collagen; fibril; procollagen-III-C-terminal propeptide; immunoassay; diagnosis; glucocorticosteroid; antibody.

97EP-00119018 97EP-00119018

31-OCT-1997; 31-OCT-1997;

06-MAY-1999. EP913692-A1

Homo sapiens

(FARB ) BAYER AG.

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The invention relates to a method of determining the rate of biosynthesis or breakdown of at least one inaccessible biological molecule in a because the subject. The method is useful for diagnosis or monitoring and treatment of diseases associated with an altered rate of biosynthesis/breakdown of an isotopically labelled precursor molecule, specifically osteoporosis; left-ventricular hypertrophy; liver cirrhosis or fibrosis, congestive theoret failure; soleroderma; coal-miner's pneumoconiosis; cardiac or lung fibrosis; Alzheimer's disease; multiple sclerosis; rheumatoid arthritis; craining and cancer. The method is also useful for screening candidate gene or protein targets, phenotypic/human validation studies on potential cycles. The present sequence is human collagen type I cross-linked carboxy terminal peptide (ICTP). This sequence is used to illustrate the
                                                                                                                                           Human; therapy; osteoporosis; left-ventricular hypertrophy; scleroderma; liver cirrhosis; congestive heart failure; multiple sclerosis; fibrosis; coal-miner's pneumoconiosis; muscle-wasting syndrome; diabetes mellitus; rheumatoid arthritis; Alzheimer's disease; muscular dystrophy; cancer; collagen type I cross-linked carboxy-terminal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determining rate of biosynthesis or breakdown of inaccessible biological molecules, useful e.g. for diagnosis or monitoring treatment, by administering labeled precursor.
                                                                                                         Human collagen type I cross-linked C-terminal peptide, PIICP(alphal).
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   AAE38640 standard; protein; 262 AA
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                                                                            (first entry)
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                                      AAE38640;
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Gaps ö 100.0%; Score 56; DB 7; Length 262; 100.0%; Pred. No. 0.43; 0; Indels Mismatches ; 11; Conservative Best Loca Matches à

1 IAGIGGEKAGG 11

RESULT 5

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(first entry) 16-JUL-1999 AAY07375; XEXAXXXX

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AAY07375 standard; protein; 270

AAY07375

Procollagen-III-C-terminal propeptide.

Diseases such as alcoholic cirrhosis, biliary cirrhosis, hepatitis, cardiac fibrosis, Crohn's disease, diabetic nephropathy constitutions caused by anyery result from an inappropriate production of and fibroses caused by anyery result from an inappropriate production of collagen fibrils. Collagen III is synthesised as a preproprotein which is fibrils are generated by cleavage of a propeptide from the C-terminus of individed by cleavage of a propeptide from the C-terminus collagen III clerminus. This sequence fibrils are formed, the PIIICP propeptide is released into the surrounding tissue fluids. The interpretate collages in immunoassay to chers which result from inappropriate collages the above diseases and chermine PIIICP concentrations and thus diagnose the above diseases and chermine PIIICP concentrations and thus diagnose the above diseases and chermine which cleases may show different levels of PIIICP in the serum so the fibrotic diseases may show different levels of PIIICP in the serum so the patient is suffering from. The new immunoassay may also be used to determine which disease a particular measure the rate of collagen synthesis in patients being treated with immunoal stochemical staining of cryostat and parifin sections to assess collagen synthesis in tissue samples from patients suspected of having fibrotic disease. New immunoassay for procollagen-III-C-terminal propeptide (PIIICP) useful for diagnosing diseases such as alcoholic cirrhosis, hepatitis and Schroeder W; Neumann R, Disclosure, Fig 1; 28pp; English Duchenne's muscular dystrophy. Burchardt ER, Kroll W, WPI; 1999-256748/22. N-PSDB; AAX57501 

Sequence 270 AA;

100.0%; Score 56; DB 2; Length 270; 100.0%; Pred. No. 0.44; 0; Indels 0; Mismatches Query Match
Best Local Similarity 100.0%

0

Gaps

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ABU70813 standard; protein; 293 AA. (first entry) 10-JUN-2003 ABU70813; RESULT 6 ABU70813

Human adipocyte Selected Interacting domain, SID, #444.

**KAXXEX** 

Human, prey, adipocyte, SID; selected interacting domain; anorectic, antidiabetic; protein-protein interaction; diabetes; yeast 2-hybrid assay; metabolic disorder; obesity.

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Query Match
Best Local Similarity
                                WPI; 2003-103412/09.
N-PSDB; ACA57357.
                        (HYBR-) HYBRIGENICS
                                                                                                            Sequence 293 AA;
      WO200286122-A2.
  Homo sapiens.
           31-OCT-2002
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Matches
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inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; cytostatic; anti arthritic; nephrotropic; anticoagulant.
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2000US-0225268P.
2000US-0225270P.
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2000US-0231243P.
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2000US-0209467P.
2000US-0214886P.
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2000US-0216647P.
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                                                                                                                  WO200155301-A2
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14-SEP-2000;
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22-AUG-2000;
22-AUG-2000;
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07-JUL-2000;
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                                                                                    Homo sapiens
                                                                                                                                                                                                                       31-JAN-2000;
                                                                                                                                                    02-AUG-2001
                The invention relates to a complex between two interacting proteins in adipocyte cells, given in the specification. The proteins are identified by selecting a bait protein from a known adipocyte marker and then by selecting a past 2-hybrid selection to isolate prey proteins encoded by members of an adipocyte cDNA library. The proteins are designated SID (RTM) (selected interacting domains) proteins. Also included are a polymorphide in the adipocyte cells, a polymorphide in the adipocyte cells, a polymorphide so f the complex, selecting a modulating compound in adipocyte comprising any of the first and adipocyte cells, a SID (RTM) polymorphide comprising any of the 738 amino acid cells, a SID (RTM) polymorlectide comprising any of the 738 mucleotide sequences given in the specification (including its fragment or variant), a SID (RTM) polymorlectide comprising any of the 738 mucleotide sequences given in the specification (including its fragment or variant), a vector comprising the vector, a protein chip comprising the polymorlectides and a recondinant host cell comprising the vector, a protein chip comprising the polymorlectides and compounds are useful for record complex, polymorphides, polymorphides much as obesity or diabetes. The polymucleotides are useful for preventing or treating metabolic disorders such as obesity or diabetes. The polymucleotides are useful as probes or primers. The complex is probes or primers. The complex is protein interacting domains (SID (RTM)) for screening drugs that medulate the protein interaction, thus complexing the therapeutic effect. The present sequence represents a SID (prey) protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                           New complex between two interacting proteins in adipocyte cells, useful for identifying selected interacting domains that modulate protein interactions, or for preventing or treating metabolic disorders such as obesity or diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 258-259; 382pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human enzyme polypeptide #761.
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                                                                                                                                                   14-MAR-2002; 2002WO-EP003768.
                                                                                                                                                                                   14-MAR-2001; 2001US-0275734P.
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14-SEP-2000; 2000US-0233065P 21-SEP-2000; 2000US-0234223P

Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder;

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20-OCT-2000; 2000US-0241785P.
20-OCT-2000; 2000US-0241785P.
20-OCT-2000; 2000US-0241786P.
20-OCT-2000; 2000US-0241786P.
20-OCT-2000; 2000US-0241809P.
20-OCT-2000; 2000US-0241809P.
20-OCT-2000; 2000US-0241809P.
20-OCT-2000; 2000US-0246474P.
08-NOV-2000; 2000US-0246474P.
08-NOV-2000; 2000US-0246474P.
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08-NOV-2000; 2000US-0246524P.
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08-NOV-2000; 2000US-024651P.
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08-NOV-2000; 2000US-0249208P.
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17-NOV-2000; 200US-024929P.
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2000US-0236369P.
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2000US-0235836P.
2000US-0236327P.
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05-DEC-2000; 2000US-0251030P.
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05-DEC-2000; 2000US-0256719P
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08-DEC-2000; 2000US-0251856P
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The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences concloding them. The erzyme polypeptides of the invention may comprise the functional classes of oxidoraclusces, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. asthma), contributed hyperproliferative disorders (e.g. asthma), contributed and disorders (e.g. AIDS) autoimmune disorders (e.g. asthma), contributed and disorders (e.g. and sorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. the encophilia), reproductive disorders (e.g. infertility) and confertious disorders (e.g. Influenza). The polymucleotides of the invention can also be used in gene therapy. AAU22915-AAU23814 represent the novel human enzyme polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but the wipo int/pub/published_pct_sequences.
                                                                                                                                                                                                                    Novel polypeptides and polynucleotides useful for diagnosing, preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; ovarian antigen; ovary disorder; breast disorder; neoplastic disorder; cancer; infectious disease; inflammatory disease; reproductive system disorder; autoimmume disorder; Alzheimer's disease; blood-related disorder; hyperproliferative disorder; hair loss; urinary system disorder; cardiovascular disorder; arthythmia; respiratory disorder; musculoskeletal system disorder; indocrine disorder; neurolity disorder; neurological disorder; endocrine disorder; gastrointestinal disorder; neurolity disorder; artifer disorder; pancreatic disorder; gastrointestinal disorder; sancreatic disorder; inherited disorder; avelopmental disorder; inherited disorder; askin aging; food additive;
                                                                                                                                                                                                                                           treating meural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.
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100.0%; Score 56; DB 4; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                        Claim 11; SEQ ID NO 1671; 1180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG60248 standard; protein; 309 AA.
                                                                                                             Rosen CA, Barash SC, Ruben SM
                                                               (HUMA-) HUMAN GENOME SCI INC.
  11-DEC-2000; 2000US-0254097P 05-JAN-2001; 2001US-0259678P
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                                                                                                                                                    WPI; 2001-465566/50.
                                                                                                                                                                             N-PSDB; AAS41545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 309 AA;
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WO200155329-A2 Homo sapiens.

02-AUG-2001.

2000US-0179065P

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The invention relates to isolated ovarian related polypeptide (ovarian antigen) comprising a sequence at least 90% identical to a sequence antigen) comprising a sequence at least 90% identical to a sequence control of a sequence (51) appearing as ABG6029-ABG60296 having protein of a sequence (51) appearing as ABG6029-ABG60296 having protein of protein of a sequence (51) appearing as ABG6023-ABG60296 having protein of protein of sequence (51) appearing a medical condition in mammalian subject of 51. Also included are the cDNA are useful for diagnosing, preventing, an anti-S1 antibody and the cDNA are useful for diagnosing, preventing, an anti-S1 antibody and the cDNA are useful for diagnosing, preventing, cappedially diseases and/or disorders of the ovary and/or breast such as ovariant Krukenberg thmour and cancel), infectious diseases (systemic lupus erythematosus, rheumatory diseases) cattoinmund disorders (systemic lupus erythematosus, rheumatory diseases) autoinmund disorders (systemic lupus erythematosus, rheumatorid arthritis), blood-related disorders (sickle cell anaemia), arthritis), blood-related disorders (sickle cell anaemia), arthritis), blood-related disorders (sickle cell anaemia), arthritis), cardiovascular disorders (shilary system disorders (arthritimias), respiratory disorders), and sorders (alsorders (alsorders (alsorders (alsorders (alsorders (alsorders (alsorders (alsorders (alsorders))), liver disorders (bilary) liver citrinois), captorders, disorders (bilary), and chonders and and inherited disorders (bilary) liver citrinois to prevent skin adjing, for preventing hair loss, to maintain organs and wound healing one for supporting cell culture of primary tissues, compliate mammalian characteristics such as body height, to modulate mammalian metabolism, to change a mammal's mental or physical state, and covarian antigen, si protein of the invention or proservative. The present sequence data for this patent did ont form part of the printed sepecification, but was contained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated human ovarian related polypeptide useful for diagnosis/treatment of disorders of ovary and breast such as neoplastic disorders, infectious diseases, inflammatory diseases, and reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; SEQ ID NO 78; 524pp; English
                                                                                                                                                                                                                                                                                                        Rosen CA, Barash SC, Ruben SM;
                                                                              04-FEB-2000; 2000US-0180628P.
07-JUN-2000; 2000US-0203467P.
14-SEP-2000; 2000US-0223398P.
17-NCV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-0250160P.
08-DEC-2000; 2000US-0251868P.
                                                                                                                                                                                                                       08-DEC-2000; 2000US-0251990P.
                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                17-JAN-2001; 2001WO-US001360
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Local 11; Conservative
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                                                                31-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders.
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Ovarian related polypeptide; neoplastic disorder; tumour; ovarian cancer; hyperproliferative disorder; adult acute lymphocytic leukaemia; breast cancer; reproductive system disorder; tuberculosis; arthritis; immune system disorder; Chediak-Higashi's syndrome; neonatal neutropenia; autoimmune disorder; Hashimoto's thyroiditis; inflammatory disorder; septic shock; multiple solerosis; central nervous system disorder; neurological disorder; allergy; Parkinson's disease; Alzheimer's disease; cardiovascular disorder; atherosclerosis; blood related disorder; respiratory disorder; uninary system disorder; musculoskeletal disorder; osteoporosis; wound healing; endocrine disorder; infectious disease; gastrointestinal disorder; transplantation; food additive; preservative.
                                                                                         Novel ovarian related polypeptide #10.
                    ABG61719 standard; protein; 309 AA
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2000US-0229513P.
2000US-0230437P.
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2000US-0214886P
2000US-0215135P
2000US-0216647P
2000US-0217487P
2000US-0217487P
2000US-0217496P
2000US-0220963P
2000US-0220963P
2000US-0220964P
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2000US-0198123P.
2000US-0205515P.
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2000US-0225214P.
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2000US-0225267P.
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                                                                    (first entry)
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05-SEP-2000; 2
06-SEP-2000; 2
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14-AUG-2000;
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14-AUG-2000;
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                                              ABG61719;
RESULT 9
              ABG61719
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Gaps

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100.0%; Score 56; DB 4; Length 309; 100.0%; Pred. No. 0.5; ive 0; Mismatches 0; Indels

1 IAGIGGEKAGG 11

58

48 IAGIGGEKAGG

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06-SEP-2000; 2000US-023124P.
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08-SEP-2000; 2000US-023124P.
08-SEP-2000; 2000US-023141P.
08-SEP-2000; 2000US-0231414P.
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08-SEP-2000; 2000US-023130P.
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14-SEP-2000; 2000US-023239P.
14-SEP-2000; 2000US-0233306P.
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14-SEP-2000; 2000US-0233306P.
25-SEP-2000; 2000US-023333P.
25-SEP-2000; 2000US-023333P.
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28-SEP-2000; 2000US-0234477P.
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20-CCT-2000; 2000US-024647P.
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2000US-0249244P.
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2000US-0249264P.
2000US-024929P.
2000US-024920P.
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2001WO-US001360
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(RUBI/) RUBIN S M.
(BARA/) BARASH S C
17-NOV-2000; 20, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 20, 17-NOV-2000; 20, 17-NOV-2000; 20, 17-NOV-2000; 20, 17-NOV-2000; 20, 17-NOV-2000; 20, 17-NOV-2000; 20, 17-NOV-2000; 20, 17-NOV-2000; 20, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV-2000; 21, 17-NOV
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Gaps

(first entry)

10-JUN-2003 ABU70735;

Human adipocyte Selected Interacting domain, SID, #366.

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polymucleotide encoding a polypeptide in the adipocyte cells, a recombinant host cell expressing at least one of the interacting recombinant host cell expressing at least one of the interacting computed in adipocyte cells, a SID (RTW) polymeptide comprising any of the 738 amino acid sequences given in the specification (including its fragment or variant), a SID (RTW) polymucleotide comprising any of the 738 nucleotide sequences given in the specification (including its fragment or variant), a vector comprising the vector, a protein chip comprising the polymeptides and a recomblex, polymeptides, polymucleotides and compounds are useful for record comprising the vector, a protein chip comprising the polymeptides and a recomblex, polymeptides, polymucleotides and compounds are useful for preventing or treating metabolic disorders such as obesity or diabetes. The polymucleotides are useful as probes or primers. The complex is particularly useful for identifying selected interacting domains (SID particularly useful for identifying selected interacting domains (SID exhibiting the therapeutic effect. The present sequence represents a SID (RTW) protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a complex between two interacting proteins in adipocyte cells, given in the specification. The proteins are identified by selecting a bait protein from a known adipocyte marker and then performing a yeast 2-hybrid selection to isolate prey proteins encoded by members of an adipocyte cDNA library. The proteins are designated SID (RTM) (selected interacting domains) proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New complex between two interacting proteins in adipocyte cells, useful for identifying selected interacting domains that modulate protein interactions, or for preventing or treating metabolic disorders such as obesity or diabetes.
                                                Human, prey, adipocyte, SID, selected interacting domain, anorectic, antidiabetic, protein protein interaction, diabetes, yeast 2-hybrid assay, metabolic disorder; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW12843 standard; peptide; 623 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 229; 382pp; English.
                                                                                                                                                                                                                                                                     14-MAR-2002; 2002WO-EP003768
                                                                                                                                                                                                                                                                                                               14-MAR-2001; 2001US-0275734P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                   Legrain P, Daviet L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                       (HYBR-) HYBRIGENICS,
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-103412/09.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ACA57279
                                                                                                                                                                                      WO200286122-A2.
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                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                              31-0CT-2002.
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AAW12843
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This sequence represents a chimeric procollagen molecule of the invention. This sequence has the procollagen C-prepropeptide from the procollagen C-prepropeptide from the procollagen C-prapropeptide from the assembly of the monomer chains into propeptide is implicated in the assembly of the monomer chains into propeptide is implicated in the assembly of the N- and C-propeptides and formation of collagen in fibril-forming pro-alpha chains. The C and formation of collagen in fibril-forming pro-alpha chains. The C they are attached. The molecule of the invention comprises a first moiety they are attached. The molecule of the invention comprises a first moiety they are attached. The bused for treatment or diagnosis in humans consult in the collagen alpha-chain or a non-collagen material. The which is an alien collagen alpha-chain or a non-collagen material. The convel collagen molecule can be used for treatment or diagnosis in humans con amimals, especially for the treatment of procollagen suicide, as an education to promote (chronic) wound healing or fibrotic diseases with reduced scarring or for use in photography, brewing, containing substitutions in the recognition site, may have significantly altered properties and characteristics, such as different binding containing or alpha-chain selection properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-propeptide; recognition sequence; procollagen; monomer chain; therapy; trimerised pro-alpha chain; fibril; procollagen suicide; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel pro:collagen mol. - comprising pro:collagen C-pro:peptide attached to an alien collagen alpha-chain or non-collagen material, useful e.g.
                                   C-propeptide; recognition sequence; procollagen; monomer chain; therapy; trimerised pro-alpha chain; fibril; procollagen suicide; wound healing; fibrotic disease; human; chimeric protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 56; DB 2; Length 623; 100.0%; Pred. No. 1; c. o, Mismatches 0; Indels
       Pro-alphal(III):(I) CP chimeric protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 32-35; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW12842 standard; protein; 626 AA.
                                                                                                                                                                                                                                                                                                                                                   (UYMA-) UNIV VICTORIA MANCHESTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Truncated pro-alpha1(III) chain.
                                                                                                                                                                                                                                                                             95GB-00017773.
                                                                                                                                                                                                                                                                                            96GB-00006152.
96GB-00012476.
                                                                                                                                                                                                                                       96WO-GB002122
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                                                                                                                                                                                                                                                                                                                                                                                           Kadler K;
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-179268/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 623 AA;
                                                                                                                             Ното варіепв
                                                                                                                                                                 WO9708311-A1
                                                                                                                                                                                                                                       30-AUG-1996;
                                                                                                                                                                                                                                                                                                                14-JUN-1996;
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                                                                                                                                                                                                                                                                                                  23-MAR-1996;
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Gaps

0; Indels

0.55;

Pred. No. 0.5 0; Mismatches

100.08;

88

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This sequence represents a truncated procollagen pro-alphal(III) chain that can be used in the procollagen molecules of the invention. The C-Droperide is implicated in the assembly of the monomer chains into trimerised pro-alpha chains prior to cleavage of the N- and C-propeptides trimerised pro-alpha chains prior to cleavage of the N- and C-propeptides of propeptides determine the type-specific assembly of the moieties to which they are attached. The molecule of the invention comprises a first moiety which is an alien collagen alpha-chain or a non-collagen meterial. The convert is an alien collagen abba-chain or a non-collagen meterial. The convert collagen molecule can be used for treatment or diagnosis in humans can mimals, especially for the treatment of procollagen suicide, as an diseases with reduced scarring or for use in photography, brewing, containing substitutions in the recognition site, may have significantly intered properties and characteristies, such as different binding containing substitutions in the recognition site, may have significantly containing substitutions in the recognition site, may have significantly containing substitutions.
                                                                                                                                                                                                                                                                                                                                                                                                        Novel pro:collagen mol. - comprising pro:collagen C-pro:peptide attached to an alien collagen alpha-chain or non-collagen material, useful e.g. for wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kinetics or alpha-chain selection properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 28-31; 69pp; English.
                                                                                                                                                                                                                                                                      (UYMA-) UNIV VICTORIA MANCHESTER
                                                                                                                                                            96WO-GB002122.
                                                                                                                                                                                                                                      96GB-00012476.
                                                                                                                                                                                                  95GB-00017773
                                                                                                                                                                                                                    96GB-00006152,
    fibrotic disease; human
                                                                                                                                                                                                                                                                                                                                                                                                      Novel pro:collagen mol.
                                                                                                                                                                                                                                                                                                            Bulleid N, Kadler K;
                                                                                                                                                                                                                                                                                                                                                WPI; 1997-179268/16.
                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT59892.
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                                                                                                                                                                                            31-AUG-1995;
23-MAR-1996;
14-JUN-1996;
                                          Homo sapiens
                                                                              WO9708311-A1
                                                                                                                                                      30-AUG-1996;
                                                                                                                  06-MAR-1997
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100.0%; Score 56; DB 2; Length 626; 100.0%; Pred. No. 1; 0; Indels 0; Mismatches Query Match Best Local Similarity 100. Matches 11; Conservative

1 IAGIGGEKAGG 11

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365 IAGIGGEKAGG 375

ADE08475 standard; protein; 842 AA. ADE08475; RESULT 13 ADE08475 

29-JAN-2004 (first entry)

Novel protein (useful for identifying genetic disorders) #630.

novel gene; novel protein; tissue marker; molecular weight marker; chromosome marker; genetic disorder.

Unidentified

WO2003054152-A2.

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The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gols; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to genetic disorders. The present amino acid sequence represents a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ren F, Zhang J, Zhao QA, Wang J;
g G, Zhou P, Drmanac RT, Wang Z;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Weng G, Zh
Boyle BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID NO 1541; 1177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT, Asundi V, Goodrich Rw,
Ghosh M, Xue AJ, Wehrman T, We
Ma Y, Wang D, Chen R, Xu C, B
                                                                                                                                                                      10-DEC-2001; 2001US-0339739P.
11-DEC-2001; 2001US-0339433P.
14-MAR-2002; 2002US-035691P.
14-MAR-2002; 2002US-035334P.
12-APR-2002; 2002US-0372381P.
                                                                                   10-DEC-2002; 2002WO-US039555.
                                                                                                                                                                                                                                                                                                                                                                                               12-APR-2002; 2002US-0372615P.
22-APR-2002; 2002US-00128558.
24-APR-2002; 2002US-0376045P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
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85 X C C C C C C C X X B Y X B Y X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X
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Sequence 842 AA;

· 0 100.0%; Score 56; DB 7; Length 842; 100.0%; Pred. No. 1.4; 0; Mismatches 0; Indels Best Local Similarity 100. Matches 11; Conservative Query Match

0

Gaps

||||||||||| 581 IAGIGGEKAGG 591 1 IAGIGGEKAGG 11

ABB50291 standard; protein; 1466 AA. ABB50291; RESULT 14 ABB50291 

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Gaps

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Collagen type III alpha-1 ovarian tumour marker protein, SEQ ID NO:72. 08-FEB-2002 (first entry)

Ovarian tumour marker gene; human; overexpression; upregulation; epithelial tumour; cancer; diagnosis; prognosis; disease monitoring; identification; serous cystadenoma; borderline serous tumour; serous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cymoderline mucinous tumour; endometrioid carcinoma; undifferentiated carcinoma; lear cell adenocarcinoma; cystadenofibroma; adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE; immune response pathway; cell proliferation regulation; protein folding; membrane localised; secreted; therapeutic target; cytostatic; gene therapy; vaccine.

Homo sapiens

WO200175177-A2.

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30-MAY-2002
                                 ABB90747;
                               RESULT 15
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An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
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                                                                                                                                                                                                          01-AUG-2001; 2001WO-US024031.
                                                                                                                                                                                                                                                                                 11-AUG-2000; 2000US-0224360P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-291856/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABL92101
                                                                                                     WO200210217-A2.
                                                         Homo sapiens.
                                                                                                                                                                                                                                                                02-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                          St Croix B,
                                                                                                                                                           07-FEB-2002.
psoriasis.
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Job time :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to methods for diagnosing and prognosing ovarian tumours in an individual via the detection and measurement of the tumours in an individual via the detection and measurement of the tumours in an individual via the detection and measurement of the expression of ovarian tumour marker genes (ABA83102-ABA83109, ABA83180, CC ABA83181 and ABA83183). The methods of the invention are useful for detecting an ovarian tumour in a patient, for identifying an individual cassessing the relative severity of ovarian cancer, in prognostic tests for a ssessing the relative severity of ovarian cancer, in tests for monitoring a patient in remission from ovarian cancer and in tests for monitoring disease status in a patient being particular tumour as The methods can additionally be used to identify a particular tumour solutionally be used to identify a particular tumour solutionally be used to identify a particular tumour selected from serous cystadenoma, borderline serous tumour, mucinous cystadenoma, borderline mucinous tumour, mucinous cystadenoma, endometriol carcinoma, undifferentiated carcinoma, clear cell adenocarcinoma, endometriol carcinoma, undifferentiated carcinoma, clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner cumour. The ovarian tumour marker genes of the invention were identified overexpressed in a broad variety of ovarian epithelial tumour cells overexpressed in a broad variety of ovarian epithelial tumour cells implicated in immune response pathways, in the regulation of cell in multiple and in protein folding, and many of these are membrane-conversed to the invention were secreted. In addition to their use as diagnostic and converse the converse of the invention and in protein folding, and many of their energy their energes of their energes or their encoded
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                                                                                                                                                                                                                                                                                                                                                Detecting and identifying ovarian tumor, identifying increased risk for developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prognostic markers, the ovarian tumour marker genes or their encoded proteins may be used as therapeutic targets for the treatment and prevention of ovarian cancer. Sequences ABB50257-ABB50299 represent proteins encoded by ovarian tumour marker genes of the invention
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                                                                                                                                                                                                                             Pizer ES, Hough CD;
                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 23; Page 114-117; 140pp; English
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                                                                       03-APR-2001; 2001WO-US010947.
                                                                                                                           03-APR-2000; 2000US-0194336P
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IAGIGGEKAGG 11
                                                                                                                                                                                                                                     Morin PJ, Sherman-Baust
                                                                                                                                                                                                                                                                                      WPI; 2001-626450/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1466 AA;
                                                                                                                                                                                                                                                                                                                    N-PSDB; ABA83117
                        11-OCT-2001
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Vogelstein B;

Kinzler KW,

2000US-0222599P.

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The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB907450 and ABB90756. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, necengligenesis in subjects bearing a vascularised tumour. prowth, necengligenesis in subjects retinopathy, rheumatoid arthritis and psoriasis Human, mouse and rat TEM retinopathy, rheumatoid arthritis and psoriasis Human, mouse and rat TEM are disclosed, as are marker oligonucleotide sequences: tumour are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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ne : 58.8824 secs
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PEM) ABL91903-ABL91995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1466 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic; normal endothelial marker; pan-endothelial marker; immunostimulant; antiangiogenic; tumour; neoangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;

Human Tumour Endothelial Marker polypeptide SEQ ID NO 226.

(first entry)

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Sequence 42, Appl
Sequence 3, Appli
Sequence 2, Appli
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 20, Appl
Sequence 40, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 28805, A
Sequence 28605, A
Sequence 28605, A
Sequence 21412, A
Sequence 21412, A
Sequence 12837, A
Sequence 12837, A
Sequence 20541, A
Sequence 20541, A
Sequence 22715, A
Sequence 22715, A
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                                                                           34. ; Search time 18.1176 Seconds (without alignments) 31.344 Million cell updates/sec
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                                                                                                                                                                                                                                                              389414
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(c) 1993 - 2004 Compugen Ltd.
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US-10-009-999A-43

US-09-029-34B-3

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US-08-963-825-21

US-08-500-811-21

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US-09-514-20

US-10-009-999A-41

US-10-009-999A-41

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US-09-252-991A-28645

US-09-252-991A-28645

US-09-252-991A-21412

US-09-489-039A-12837

US-09-489-039A-12837

US-09-489-039A-12837

US-09-252-991A-32499

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US-09-252-991A-32499

US-09-252-991A-32499

US-09-252-991A-3027

US-09-252-991A-32499
                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                    389414 segs, 51625971 residues
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                                                                              September 18, 2004, 04:20:54
                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                            length: 0
length: 2000000000
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56
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Match Length DB
           Copyright
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Maximum DB seq
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                                                        OM protein
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                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                       Searched:
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No.
                                                                                    Run on:
                                                                                                                                          Title:
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		, 0
Sequence 21790, A Sequence 28570, A Sequence 16765, A Sequence 17, Appl Sequence 54, Appl Sequence 54, Appl Sequence 54, Appl Sequence 54, Appl Sequence 54, Appl Sequence 54, Appl Sequence 54, Appl Sequence 18076, A Sequence 18076, A Sequence 18076, A Sequence 18076, A Sequence 18076, A Sequence 18076, A Sequence 180, Appl Sequence 18	COLLAGEN RESORPTION ASSAYS	<pre>ig to carboxy-terminal type III collagen Length 11; Indels 0; Gaps</pre>
US-09-252-991A-21790 US-09-252-991A-28570 US-09-225-991A-16765 US-08-924-629C-17 US-08-924-629C-17 US-08-937-362-54 US-08-997-362-54 US-08-997-362-54 US-08-97-362-54 US-09-095-855-54 US-09-097-855-54 US-09-205-426-54 US-09-206-426-54 US-09-206-426-54 US-09-252-991A-18076 US-09-252-991A-18076 US-09-252-991A-18076 US-09-252-991A-18076 US-09-252-991A-18076 US-09-252-991A-18076 US-09-072-596-1184 US-09-072-596-1184	ALIGNMENTS 009999A 210/009,999A 223,0099935,098 60/141,574 60/142,675 09/385,740	peptide corresponding de sequence of human ty Score 56, DB 4; Le; Pred. No. 0.0077; O; Mismatches 0;
4         4         4         0	1/100 120 120 120 120 120 120 120	etic eptic 0.0%
9833 92110 92111 932444444444444444444444444444444444444	pplication US/10 2980 2980 2980 2980 2980 2980 2980 298	o sapiens C FEATURE TION: synthetic p. TION: telopeptide 100.0%; Conservative 0 GGEKAGG 11
@ @ @ @ @ @ @ @ @ @ @ @ @ @ @ @ @ @ @	ALI.  1-999A-42  No. 660290  INTROMATION:  INTROMATION:  PANT: EXPE, David R.  OF INVENTION: SYNTHETIC PEPTID  UNTENTION: SYNTHETIC PEPTID  UNTENTION: SYNTHETIC PEPTID  UNTENTION: SYNTHETIC PEPTID  UNTENTION: SYNTHETIC PEPTID  UNTENTION: SYNTHETIC PEPTID  UNTENTION: SYNTHETIC PEPTID  UNTENTION: SYNTHETIC PEPTID  UNTENTION: SYNTHETIC PEPTID  UNTENTION: SYNTHETIC PEPTID  UNTENTION: SYNTHETIC PEPTID  UNTENTION: SYNTHETIC PEPTID  APPLICATION NUMBER: US 60/142, PILING DATE: 1999-06-29  APPLICATION NUMBER: US 60/142, PILING DATE: 1999-07-07  ROFILING DATE: 1999-07-07  ROFILING DATE: 1999-07-07  ROF SEQ ID NOS: 45  NO 42  HILLING DATE: 1999-08-30  ROF SEQ ID NOS: 45  NO 42	# 12 44 44 44 44 44 44 44 44 44 44 44 44 44
$egin{array}{c} \mathcal{L} \mathcal{L} \mathcal{L} \mathcal{L} \mathcal{L} \mathcal{L} \mathcal{L} L$	999A- 42, 66 NFOB NFOB NFOB NFOB NFOB NFOB NFOB NFOB	PRI SSN: HG SSN: HG EY: M: INFORI 1999A itch 11;
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1  US-10-009-999A-42  Sequence 42, Application US/1; Sequence 42, Application US/1; Patent No. 660290  GENERAL INFORMATION:  TITLE OF INVENTION: FILE REFERENCE: WROS-1-18220  CURRENT FILING DATE: 2003-0  PRIOR APPLICATION NUMBER: PC  PRIOR FILING DATE: 1999-12-1  PRIOR FILING DATE: 1999-12-1  PRIOR FILING DATE: 1999-16-1  PRIOR FILING DATE: 1999-16-1  PRIOR FILING DATE: 1999-16-1  PRIOR FILING DATE: 1999-06-1  PRIOR FILING DATE: 1999-07-0  PRIOR FILING DATE: 1999-07-0  PRIOR FILING DATE: 1999-07-0  PRIOR FILING DATE: 1999-07-0  PRIOR FILING DATE: 1999-07-0  PRIOR FILING DATE: 1999-07-0  PRIOR FILING DATE: 1999-07-0  PRIOR FILING DATE: 1999-07-0  PRIOR FILING DATE: 1999-07-0  PRIOR FILING DATE: 1999-07-0  PRIOR PLILING DATE: 1999-07-0  PRIOR PLILING DATE: 1999-07-0  PRIOR PLILING DATE: 1999-08-1  SOFTWARE: PALENTENTENTENTENTENTENTENTENTENTENTENTENTE	; TYPE: PKI ; ORGANISM: HOMO ; FEATURE: ; NAME/KEY: NISC, ; OTHER INFORMAT ; OTHER INFORMAT US-10-009-999A-42 Query Match Best Local Simil Matches 11; C QY 1 IAGI

Sequence 43, Application US/10009999A
Sequence 43, Application US/10009999A
Patent No. 6602980
GENERAL INPORMATION:
GENERAL INPORMATION:
TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS

US-10-009-999A-43

RESULT 2

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FILING DATE:
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US-08-963-825-21
                                                                                                                    SEQ ID NO 2
LENGTH: 626
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                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                              FEATURE:
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OTHER INFORMATION: synthetic peptide corresponding to carboxy-terminal
OTHER INFORMATION: telopeptide sequence of human type III collagen
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CTHER INFORMATION: Description of Artificial Sequence: SEQUENCE;
OTHER INFORMATION: DERIVED FROM CDNA OF PROCOLLAGENS
US-09-029-348-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 100.0%; Score 56; DB 4; Length 12; all Similarity 100.0%; Pred. No. 0.0084; 11; Conservative 0; Mismatches 0; Indels
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Patent No. 6171827
GENERAL INFORMATION:
APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER
ITLE OF INVENTION: NOVEL PROCOLLAGENS
FILE REPRESENCE: 008957902 ILSTING
CURRENT APPLICATION NUMBER: US/09/029, 348
CURRENT FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
             CURRENT APPLICATION NUMBER: US/10/009,999A
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: UCT/US99/29357
PRIOR FILING DATE: 1999-12-10
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: US 60/141,574
PRIOR APPLICATION NUMBER: US 60/141,574
PRIOR PILING DATE: 1999-06-29
PRIOR PILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: US 60/142,675
PRIOR APPLICATION NUMBER: US 60/142,675
PRIOR APPLICATION NUMBER: US 09/385,740
PRIOR FILING DATE: 1999-07-07
PRIOR PRIOR DATE: 1999-07-07
PRIOR PRILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 45
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ORGANISM: Artificial Sequence
FILE REFERENCE: WROS-1-18220
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Best Local Similarity
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Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 43
LENGTH: 12
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Sequence 21, Application US/08963825

Patent No. 6110689

GENERAL INFORMATION:
APPLICANT: GVist, Per
APPLICANT: Bonde, Martin

TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEGUENCES: 21

CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: SEQUENCE OTHER INFORMATION: DERIVED FROM cDNA OF PROCOLLAGENS US-09-029-348-2
                                                                                                                                                                                                                                                                                                                             100.0%; Score 56; DB 3; Length 626; 100.0%; Pred. No. 0.37;
                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/963,825
                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                     CURRENT APPLICATION NUMBER: US/09/029,348 US/08/029,348 TILING DATE: 1998-05-07 NUMBER OF SEQ ID NOS: 20 SOFTWARE: PATENTIN VEY. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/187,319
FILING DATE: 21-7AN-1994
ATTORNEY/AGENT INFORMATION:
NAME: GGOOTIE, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECHONE: 212-527-7700
TELECHAX: 212-527-7700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
FILE REFERENCE: d087857PUS LISTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Home sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212-7-2
TELEFAX: 236687
TELEFAX: 236687
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Darby & Darby PC
                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 11; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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US-08-963-825-21

Sequence 2, Application US/09029348
Patent No. 6171827
GENERAL INFORMATION:
APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER
ITLE OF INVENTION: NOVEL PROCOLLAGENS

US-09-029-348-2

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A Method for Assaying Collagen Fragments in Body Fluids, A Test Kit and Means for Carrying Out the Method and Use of the Method to Diagnose the Presence of Disorders Associated with the Metabolism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21, Application US/09548608

Patent No. 6355442

GENERAL INFORMATION:
APPLICANT: Ovist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence
TITLE OF INVENTION: Disorders Associated with the Metabolism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 1078;
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC Compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/09/570,573
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 50; DB 4
Pred. No. 5.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4305/08701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COLLAGEN ALPHA 1 (III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: GGGOTIS, Adda C
REGISTRATION NUMBER: 29.714
REFERENCE/DOCKET NUMBER: 4305
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFRAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
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805 Third Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Darby & Darby
STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 90.9%;
Matches 10; Conservative
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Patent No. 6342361
GENERAL INFORMATION:
APPLICANT: Qvist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method
TITLE OF INVENTION: Method
TITLE OF INVENTION: Disorde
TITLE OF INVENTION: Disorde
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein ORIGINAL SOURCE: ORRANGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1058 IAGIGAEKAGG 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 236687
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IAGIGGEKAGG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                     STREET: 805 Thire
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-09-548-608-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
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                                                                                                                                                                                                                                                                                                                              APPLICANT: Qvist, Per APPLICANT: Qvist, Per APPLICANT: Qvist, Per APPLICANT: Bonde, Martin TITLE OF INVENTION: A Method for Assaying Collagen Fragments TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of NUMBER OF SEQUENCES: 21
CORRESPONDENCE 3.
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                    Gaps
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                        Score 50; DB 3; Length 1078;
Pred. No. 5.3;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,811
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29,714
FP: 4305/08701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 7
US-09-570-573-21
; Sequence 21, Application US/09570573
                                                                                                                                                                                                                                                US-09-500-811-21
; Sequence 21, Application US/09500811
; Patent No. 6333314
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GGOOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305
TELECOMMUNICATION INFORMATION:
TELECHONE: 212-527-7700
TELEPAK: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 21
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
                                 89.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1058 IAGİGAEKAĞĞ 1068
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                                                                                                                                                           1058 IAGIGAEKAGG 1068
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IAGIGGEKAGG 11
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                                                                                                                   1 IAGIGGEKAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 10; Conserv
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                                                   Local Similarity
es 10; Conserv
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New York
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                               Query Match
Best Local &
                                                                           Matches
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New York

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** APPLICANT: BYCE, David R.

** APPLICANT: BYCE, David R.

** TITLE OF INVENTION: SYNTHEFIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS
FILE REFRENCE: WROS-1-1820

** CURRENT APPLICATION NUMBER: US/10/009, 999A

** CURRENT PILING DATE: 2003-01-22

** PRIOR APPLICATION NUMBER: PCT/US99/29357

** PRIOR APPLICATION NUMBER: US 69/335,098

** PRIOR FILING DATE: 1999-06-17

** PRIOR PILING DATE: 1999-06-29

** PRIOR PILING DATE: 1999-06-29

** PRIOR PILING DATE: 1999-06-29

** PRIOR PILING DATE: 1999-06-30

** PRIOR PILING DATE: 1999-07-07

** PRIOR PILING DATE: 1999-07-07

** PRIOR PILING DATE: 1999-07-07

** PRIOR PILING DATE: 1999-07-07

** PRIOR PILING DATE: 1999-08-30

** NUMBER OF SEQ ID NOS: 45

** SOPTHARE: PATENTIN VERSION 3.2

** SOPTHARE: PATENTIN VERSION 3.2

** SOPTHARE: PATENTIN VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: synthetic peptide corresponding to carboxy-terminal OTHER INFORMATION: telopeptide sequence of human type III collagen
                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Patent No. 6602980
GENERAL INFORMATION:
APPLICANT: Byre, David R.
ITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS
                                                                                                                                                                                                                                                                                                                                                                        ·,
                                                                                                                                                                                                                                                                                                                         Length 15;
                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                                                                                                                                                         DB 4;
. 0.18;
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 40, Application US/10009999A; Patent No. 6602980; GENERAL INFORMATION:
REFERENCE/DOCKET NUMBER: 94
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 354-4642
TELEFAX: (415) 354-4752
                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-278-774-20
                                                                                                                                                                                                                                                                                                                                                                                                           3 GIGGEKAGG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MISC FEATURE
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US-10-009-999A-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/08278774

Patent No. 6653450

GENERAL INFORMATION:
APPLICANT: Berg, Richard A
APPLICANT: Toman, David P
APPLICANT: Toman, David P
APPLICANT: Wallace, Donald
TITLE OF INVENTION: MUTATED RECOMBINANT COLLAGENS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSER: COLLAGEN CORPORATION
STREET: 2500 Faber Place
CITY: Palo Alto
COUNTRY: USA
                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/548,608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/278,774
FILING DATE: 22-UUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GGGOTIS, Adda C.
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECHOMENICATION INFORMATION:
TELEPHONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARATERISTICS:
LENGTH: 1078 amino acids
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NAME: Rafayko, Kathi L
REGISTRATION NUMBER: 36,644
                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IAGIGGEKAGG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-548-608-21
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RESULT 9

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TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Pred. No. 62;
             FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28805
LENGTH: 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 62;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                        Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa
                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28805
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70.0%;
                                                                                                                                                                                                                                                                                                                                        73.2%;
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 63...
7; Conservative
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186 IAALGGEQSGG 196
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Matches 7; Conserv
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/EX. MISC.FEATURE
OTHER INFORMATION: SYLCHOLIC peptide corresponding to carboxy-terminal
OTHER INFORMATION: telopeptide sequence of human type III collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: EXRE, DAVID R.

APPLICANT: EXRE, DAVID R.

TITLE OF INVENTION: ANTIGEN-BINDING FRACKENTS OF AN ANTIBODY

TO TYPE-I COLLAGEN AMINO-TERMINAL TELOPEPTIDE

NUMBER OF SEQUENCES: 30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/221,705

FILING DATE: 01-APR-1994

PRIOR APPLICATION DATE:

APPLICATION NUMBER: 614,719

FILING DATE: 21-007-1990

APPLICATION NUMBER: 444,881

FILING DATE: 01-DEC-1989

APPLICATION NUMBER: 118,234

FILING DATE: 06-NOV-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75.0%; Score 42; DB 4; Length 9; 100.0%; Pred. No. 3e+05; tive 0; Mismatches 0; Indels
         FILE REFERENCE: WROS-1-18220
CURRENT APPLICATION NUMBER: US/10/009,999A
CURRENT FILING DATE: 203-01-22
RUNCA APPLICATION NUMBER: PCT/US99/29357
PRIOR FILING DATE: 1999-12-10
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: US 60/142,274
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/142,675
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
SEQID NUMBER OF SEQID NOS: 45
SEQID NOS: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 28805, Application US/09252991A ; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GIGGEKAGG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 8; Conserv
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Matches 8; Conserv
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;Patent No. 5473052
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Sequence 23643, Application US/09252991A

Sequence 23644, Application US/09252991A

Fatent No. 6551795

GENERAL INFORMATION:
MARC GENERAL INFORMATION:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ACRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ACRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ACRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ACRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

THE REFERENCE: 107196-136

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR SEQ ID NOS: 33142

SEQ ID NO 23643

LENGTH: 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26476, Application US/09252991A

Sequence 26476, Application US/09252991A

Sequence 26476, Application US/09252991A

Sequence 26476, Application US/09252991A

Sequence 26476, Application US/09252991A

PRIOR PILIATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERCGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-7

NUMBER OF SEQ ID NOS: 33142
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Length 221;
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                                                                 1; Indels
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; TYPE: PRT ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-26476

0; Gaps Query Match 71.4%; Score 40; DB 4; Length 674; Best Local Similarity 63.6%; Pred. No. 1.2e+02; Matches 7; Conservative 2; Mismatches 2; Indels

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1 IAGIGGEKAGG 11 | :||:||| 410 ITWVGGDKAGG 420

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Search completed: September 18, 2004, 04:32:23 Job time : 19.1176 secs

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Sequence 19, Appl
Sequence 78, Appl
Sequence 226, Appl
Sequence 72, Appl
Sequence 33, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 103, Appl
Sequence 103, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
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Sequence 43, Appl
Sequence 11, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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67.677 Million cell updates/sec
                                                                September 18, 2004, 04:29:56; Search time 52.1961 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                       1342398
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-615-959-43
US-10-366-125-11
US-00-908-711-78
US-09-908-711-78
US-09-918-715-226
US-09-918-715-226
US-10-177-293-68
US-10-357-81-3
US-10-357-81-3
US-10-357-81-3
US-10-358-024-3
US-10-358-024-3
US-10-402-018-12-3
US-10-402-018-12-3
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US-10-688-124-113
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                                                                                                                                                                                      1342398 seqs, 321133274 residues
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Maximum Match 100%
Listing first 45 summaries
                                           OM protein - protein search, using sw model
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Match Length DB
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Sequence 4, Appli Sequence 6, Appli Sequence 4, Appli	106(	Sequence 41, Appl Sequence 196331, Sequence 139908.		Sequence 114393, Sequence 37899, A		Sequence 3/950, A Sequence 128057,	Sequence 47773, A	70808,	_	Sequence 189506, Sequence 253049.	equence	11462	180655	equence 363,	55247	Sequence 142586,	1669	Sequence 51, Appl
10-402 10-402 10-402	10-437- 10-615-	US-10-615-959-41 US-10-437-963-196331 US-10-437-963-139908	0-437-963-1	US-10-437-963-114393 US-10-425-114-37899	US-10-767-701	US-10-425-114- US-10-437-963-	US-10-4	US-10-425-114-	US-10-425-114-	US-10-437-963-189506 US-10-424-599-253049	US-10-425-114-	US-10-437-96	US-10-437-963-18	US-09-975-719-	US-10-425-114-55247	US-10-437-963-1425	US-10-437-963-	US-09-975-719-51
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16 17 18	19 20 21	23 2	255	27.	56	30 31	32	3.4	32	36	88	39	40	41	42	43	44	45

# ALIGNMENTS

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US-10-615-959-42

US-10-615-959-42

Sequence 42, Application US/10615959

Publication No. USZO40048321A1

SEGUENCE 42, INFORMATION:
GENERAL INFORMATION:
APPLICANT: Eyre, David R.

TITLE OF INVENTION:
TITLE OF INFORMATION:
CURRENT APPLICATION NUMBER: US/10/615,959

CURRENT FILING DATE: 2003-07-08

PRIOR PELLOR DATE: 2003-01-22

PRIOR PELLOR DATE: 12003-01-22

PRIOR PELLOR OF INTERNATION NUMBER: US/10/009,993A

PRIOR PELLOR OF INTERNATION NUMBER: US/10/009,993A

PRIOR PELLOR DATE: 1999-12-10

PRIOR PELLOR DATE: 1999-06-17

PRIOR PELLOR DATE: 1999-06-17

PRIOR PELLOR DATE: 1999-06-17

PRIOR PELLOR DATE: 1999-06-17

PRIOR PELLOR DATE: 1999-06-17

PRIOR PELLOR DATE: 1999-06-17

PRIOR PELLOR DATE: 1999-07-07

PRIOR PELLOR DATE: 1999-07-07

PRIOR PELLOR DATE: 1999-08-30

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PATENTING DATE: 1999-08-30

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PATENTING PATE: 1999-08-30

OCHER INFORMATION: EXPIRECT PEATURE

OCHER INFORMATION: EXPIRECT PEATURE

OTHER INFORMATION: telopeptide sequence of human type III collagen

US-10-615-959-42
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Query Match 100.0%; Score 56; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.035;

us-10-615-959-42.rapb

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TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS
FILE REPERENCE: WOOS-1-1820
CURRENT APPLICATION NUMBER: US/10/615,959
FUND PELICATION NUMBER: US/10/009,999A
PRIOR FLILING DATE: 1090-10-22
PRIOR PLILING DATE: 1090-10-22
PRIOR FLILING DATE: 1090-10-22
PRIOR FLILING DATE: 1090-6-17
PRIOR FILING DATE: 1090-6-17
PRIOR FILING DATE: 1090-6-29
PRIOR FILING DATE: 1090-6-29
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PRIOR FILING DATE: 1090-6-29
PRIOR FILING DATE: 1090-6-20
PRIOR FILING DATE: 1090-6-20
PRIOR FILING DATE: 1090-6-20
PRIOR SEQ ID NOWBER: US 60/142,675
PRIOR FILING DATE: 1090-6-20
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NAME/KEY: MISC_FEATURE
OTHER INFORMATION: synthetic peptide corresponding to carboxy-terminal
OTHER INFORMATION: telopeptide sequence of human type III collagen
        Gaps
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      Indels
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    Mismatches
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Publication No. US20040048321A1
GENERAL INFORMATION:
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; Publication No. US20030228259A1
; GENERAL INFORMATION:
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  11; Conservative
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                                       1 IAGIGGEKAGG 11
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ORGANISM: Homo sapiens
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Matches
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APPLICANT: Hellerstein, Marc
TITLE OF INVENTION: MEASUREMENT OF BIOSYNTHESIS AND BREAKDOWN RATES OF
TITLE OF INVENTION: BLOGGICAL MOLECULES THAT ARE INACCESSIBLE OR NOT
TITLE OF INVENTION: BLOGGICAL MOLECULES THAT ARE INACCESSIBLE OR NOT
TITLE OF INVENTION: BLOGGICAL MOLECULES THAT ARE INACCESSIBLE OR NOT
TITLE OF INVENTION: BY LABEL INCORPORATION INTO METABOLIC DERIVATIVES AND
FILE REFERENCE: 41627203300
CURRENT APPLICATION NUMBER: US 10/366,125
PRIOR FILING DATE: 2003-02-12
PRIOR FILING DATE: 2003-02-12
PRIOR FILING DATE: 2002-02-12
SPRIOR FILING DATE: 2003-02-02-12
SEQ ID NOS: 28
SOFTWARE: FASEED for Windows Version 4.0
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GENERAL INFORMATION:

APPLICANT: ROSeen et al.

TITIE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PAL28

CURRENT APPLICATION NUMBER: US/09/908,711

CURRENT FILING DATE: 2001-07-20

PRIOR PILING DATE: 2001-01-17

PRIOR PILING DATE: 2001-01-17

PRIOR APPLICATION NUMBER: US/10/1344

PRIOR PILING DATE: 2001-01-17

PRIOR APPLICATION NUMBER: US/1/01344

PRIOR APPLICATION NUMBER: US/1/01345

PRIOR APPLICATION NUMBER: US/1/01345

PRIOR APPLICATION NUMBER: US/1/01345

PRIOR APPLICATION NUMBER: US/1/01345

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PRIOR APPLICATION NUMBER: US/1/01345

PRIOR APPLICATION NUMBER: US/1/01329

PRIOR APPLICATION NUMBER: US/1/01329

PRIOR PILING DATE: 2001-01-17

PRIOR APPLICATION NUMBER: US/1/01329

PRIOR PILING DATE: 2001-01-17

PRIOR PILING DATE: 2001-01-17

PRIOR APPLICATION NUMBER: US/1/01329

PRIOR PILING DATE: 2001-01-17
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                                                                                   100.0%; Score 56; DB 15; 100.0%; Pred. No. 0.079;
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APPLICATION NUMBER: US01/01354
FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 19, Application US/10366125; Publication No. US20030228259A1; GENERAL INFORMATION:
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Patent No. US20020045230A1
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                                                                                                          l Similarity 100.0%;
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Best Local Similarity 100.
Matches 11, Conservative
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; ORGANISM: Homo sapiens
US-10-366-125-11
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US-10-366-125-19
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                                                                                                               Best Local Similarity
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                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 11; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                             APPLICANT: BEAG SC. CIOIX
APPLICANT: BEAG SC. CIOIX
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2000-08-01
PRIOR PILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-04-11
SPRIOR FILING DATE: 2000-04-11
SPRIOR FILING DATE: 2000-04-11
SPRIOR FILING DATE: 2000-04-11
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SPRIOR FILING DATE: 2000-04-11
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SPRIOR FILING DATE: 2000-04-11
SPRIOR PAPLICATION NUMBER: 60/282,850
PRIOR PAPLICATION NUMBER: 60/282,850
SPRIOR DATE: 2000-04-11
SPRIOR PAPLICATION NUMBER: 60/282,850
SPRIOR DATE: 2000-04-11
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SPRIOR DATE: 2000-04-11
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Sequence 72, Application US/10257021
Sequence 72, Application US/10257021
Sequence 72, Application Wo. US20030211498A1
Sequence 72, Application Worlin, Partice J.
APPLICANT: Morin, Farrice J.
APPLICANT: Picer, Ellen S.
APPLICANT: Picer, Ellen S.
APPLICANT: Picer, Ellen S.
APPLICANT: Poger, Colleen D.
TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER
FILE REFERENCE: 14014.03569U2
CURRENT APPLICATION NUMBER: US/10/257,021
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: 60/194,336
PRIOR PILING DATE: 2001-04-03
PRIOR PILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 147
SOFTWARE: REAUSEQ for Windows Version 4.0
SEQ ID NO 72
                                                                                                                                                                            Sequence 226, Application US/09918715
Publication No. US20030017157A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||||||||||
1205 IAGIGGEKAGG 1215
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Best Local Similarity 100.
Matches 11; Conservative
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                           1 IAGIGGEKAGG 11
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TYPE: PRT
ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-09-918-715-226
                                                                                                                                  RESULT 6
US-09-918-715-226
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US-10-257-021-72
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NAME/KEY: SITE
LOCATION: (2)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (4)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US01/01341
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,856
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01312
PRIOR FILING DATE: 2001-01-17
PRIOR PILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-01-31
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-06-07
PRIOR PILING DATE: 2000-06-07
PRIOR PILING DATE: 2000-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                R APPLICATION NUMBER: 09/764,853

R FILING DATE: 2001-01-17

R APPLICATION NUMBER: US01/01349

R FILING DATE: 2001-01-17

R APPLICATION NUMBER: 09/764,902

R FILING DATE: 2001-01-17

R APPLICATION NUMBER: 09/764,870

R FILING DATE: 2001-01-17

R APPLICATION NUMBER: US01/01348

R FILING DATE: 2001-01-17

R APPLICATION NUMBER: US01/01348

R FILING DATE: 2001-01-17

R APPLICATION NUMBER: US01/01348

R FILING DATE: 2001-01-17

R APPLICATION NUMBER: US01/01347

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R APPLICATION NUMBER: US01/01347

R FILING DATE: 2001-01-17
                                                                                   R FILING DATE: 2001-01-17

R APPLICATION NUMBER: 09/764,869

R PILING DATE: 2001-01-17

R APPLICATION NUMBER: 0801/01340

R FILING DATE: 2001-01-17

R FILING DATE: 2001-01-17

R FILING DATE: 2001-01-17

R APPLICATION NUMBER: 09/764,874

R APPLICATION NUMBER: US01/01334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: USO1/01307
FILING DATE: 2001-01-17
APPLICATION NUMBER: 09/764,864
FILING DATE: 2001-01-17
APPLICATION NUMBER: USO1/01341
                                                                                                                                                                                                                                                                                                FILING DATE: 2001-01-17
APPLICATION NUMBER: 09/764,898
FILING DATE: 2001-01-17
APPLICATION NUMBER: US01/01320
FILING DATE: 2001-01-17
                                      FILING DATE: 2001-01-17
APPLICATION NUMBER: US01/01339
           09/764,891
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SEQ ID NO 78
LENGTH: 309
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Best Local Similarity
Matches 11; Conserv
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Gaps .. 0

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11; Conservative

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US-10-357-851-3

Sequence 3, Application US/10357851

Publication No. US20040151731A1

GENERAL INFORMATION:

APPLICANT: Jicha, Douglas L.

ITILE OF INVENTION: Method and Compositions Involving

TITLE OF INVENTION: T-Lymphocyte Reactivity with Collagen in Aortic Tissue of

TITLE OF INVENTION: Abdominal Aortic Aneurysm Patients

FILE REFERENCE: 13376US

CURRENT FILING DATE: 2003-02-04

NUMBER OF SEQ ID NOS: 3

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NOS: 3
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| Publication No. US20040151732A1
| Publication No. US20040151732A1
| GENERAL INFORMATION:
| APPLICANT: Pelsue, Stephen
| TITLE OF INVENTION: Methods and Compositions Involving Blood
| TITLE OF INVENTION: T-Lymphocytes Reactivity with Collagen
| TITLE OF INVENTION: UNMBER: US/10/358,024
| CURRENT FILING DATE: 2003-02-04
| NUMBER OF SEQ ID NOS: 3
| SOFTWARE: FastSEQ for Windows Version 4.0
| LENGTH: 1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 56; DB 14; Length 1466; 100.0%; Pred. No. 4.6;
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THERAPY OF COLON CANCER
                FILE REFERENCE: MPHOI-029P2RNM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
FRIOR APPLICATION NUMBER: US 60/339,971
FRIOR FILING DATE: 2001-12-10
FRIOR FILING DATE: 2002-03-05
FRIOR PELING DATE: 2002-03-05
FRIOR PELING DATE: 2002-03-05
FRIOR FILING DATE: 2002-05-20
NUMBER: OF SEQ ID NOS: 228
SEQ ID NO 33
LENGTRARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 1466
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo Sapiens
US-10-301-822-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1466
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US-10-358-024-3
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APPLICANT: Mils, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-038
CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT FILING DATE: 2002-06-21
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Sequence 33, Application US/10301822
Sequence 33, Application US/10301822
Sequence 33, Application US/10301822
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Burgart, Lawrence J.
APPLICANT: Burgart, Lawrence J.
APPLICANT: MINVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
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100.0%; Score 56; DB 14; Length 1466;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 11; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR FILING DATE: 2001-06-21
PRIOR FILING DATE: 2001-06-27
PRIOR FILING DATE: 2001-06-27
PRIOR FILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-06-27
PRIOR PILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2002-05
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                      Xu, Yongyao
Hoersch, Sebastian
Monahan, John
Meyers, Rachel E.
Bast Jr., Robert C.
Hortobagyi, Gabriel N.
Pusztai, Lajos
Meric, Funda
                                                                                                                                                                                                                 Gannavarpu, Manjula
Kamatkar, Shubhangi
Mertens, Maureen
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                                                                                                                                                                                                                                                                                               Myer, Vic
Wang, Youzhen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IAGIGGEKAGG 11
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US-10-177-293-68
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APPLICANT:
APPLICANT:
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NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELEPHONE: 212-527-7700
TELEPHONE: 212-753-6237
TELEPA: 236687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/058,124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/570,573
FILING DATE: 2002-MAY-12
APPLICATION NUMBER: 08/187,319
FILING DATE: «UNKNOWN:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 29-Jan-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21, Application US/10058124 Publication No. US20030119058A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   98.2%;
90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Martin
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Bonde, Mart
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                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 98.2
Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                SEQ ID NO 12
LENGTH: 1466
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                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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Publication No. US20040005663A1

GENERAL INFORMATION:
APPLICANT: Bell, Marcum P.
APPLICANT: Neff, Thomas B.
APPLICANT: Polarek, James W.
APPLICANT: Seeley, Todd W.
TILLE REFERENCE: FP0402.3 CON
CURRENT APPLICATION NUMBER: US/10/402,089
CURRENT FILING DATE: 2003-03-26
PRIOR FILING DATE: 2003-110
NUMBER: OF SEQ ID NOS: 72
                                                                                                                                                                                                                                                              Sequence 103, Application US/10734564
; Publication No. US20040157278A1
; GENERAL INFORMATION:
; APPLICANT: Christopher C Burgess et al
; TITLE OF INVERTION: Detection Methods Using TIMP1
; TITLE OF INVERTION: Detection Methods Using TIMP1
; CURRENT APPLICATION UNDER: US/10/734,564
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: FRAESEQ for Windows Version 4.0
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                                                                                                 0; Mismatches
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                                                           100.0%; Score 56; 100.0%; Pred. No.
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SEQ ID NO 12
LENGTH: 1466
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                                                           Query Match 100.
Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                       1 IAGIGGEKAGG 11
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; ORGANISM: Homo Sapien
US-10-358-024-3
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US-10-402-089-12
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US-10-402-072A-12
                                                                                                                                                                                                                                  RESULT 12
US-10-734-564-103
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LENGTH: 1466
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ò g Best Loca Matches

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TITLE OF INVENTION: A Method for Assaying Collagen Fragments in Body Fluids, A Test Kit and Means for Carrying Out Method and Use of the Method to Diagnose the Presence Disorders Associated with the Metabolism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Pred. No. 6.5;
1; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
Sequence 12, Application US/10402072A
Publication No. US20040018592A1
GENERAL INFORMATION:
APPLICANT: Bell, Marcum P.
APPLICANT: Bell, Thomas B.
APPLICANT: Selarek, James W.
APPLICANT: Seeley, Todd W.
TITIE OF INVENTION: BOVINE COLLAGENS AND GELATINS
FILE REFERENCE: FP0402.2 COM
CURRENT APPLICATION NUMBER: US/10/402,072A
CURRENT FILING DATE: 2003-03-05
PRIOR APPLICATION NUMBER: US 09/709,700
PRIOR RILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn version 3.2
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the of

 Query Match
 89.3%;
 Score 50;
 DB 14;
 Length 1078;

 Best Local Similarity
 90.9%;
 Pred;
 No. 28;

 Matches 10;
 Conservative
 0;
 Mismatches
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 Indels
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Search completed: September 18, 2004, 04:56:13 Job time : 52.1961 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 18, 2004, 04:02:05 Run on:

% Search time 13.3725 Seconds (without alignments) 79.125 Million cell updates/sec

US-10-615-959-42 56 1 IAGIGGEKAGG 11 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 segs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### STIMMARTES

	Description	alpl	collagen alpha 1(I	collagen alpha 1(I	heat shock protein	probable folylpoly	arylesterase [impo	a)	PBSX prophage ORF	formylmethanofuran	formylmethanofuran	hypothetical prote			hypothetical prote	homeobox protein -	hypothetical prote		halocyanin precurs	circumsporozoite p	protein F21H11.3 [	leucine aminopepti	hypothetical glyci	$\sim$	_	_	Н		ä	hypothetical prote
SUMMARIES		CGHU7L	S41067	S59856	S14998	F70863	AE2981	C98302	F69732	H69074	S57457	E95286	T51035	T14302	T47394	149754	H70599	T08002	F84274	OZZOAL	B88450	D83167	F70971	H95240	A99705	T00148	T30023	T29390		AI1951
	DB	-	~	N	7	N	~	~	Ŋ	N	N	N	~	2	7	~	~	7	N	Н	~	7	~	~	~	~	~	~1	~	0
	Length	1466	636	1464	161	487	209	209	1332	270	270	298	548	87	163	399	846	151	205	378	423	495	588	605	605	694	875	935	1545	N
•	Query Match	100.0	92.9	92.9	78.6	78.6	75.0	75.0	73.2	71.4	71.4	71.4	71.4	9.69	θ.	9.69	9.69	67.9	۲.	•	67.9	7.	7.		7.	7.	۲.	67.9	7.	66.1
	Score	26	52	52	44	44	42	42	41	40	40	40	40	39	39	39	39	38	38	38	38	38	38	38	38	38	38	38	38	37
			7	e	4	5	9	7	<b>6</b> 0	6	10	11	12	13	14	15	16	17		19	20	21	22	23	24	25	56	27	28	29

A; Accession: S04887
A; Molecule type: mRNA
A; Residues: 149-163, 'G', 164-240, 'D', 242-471, 'D', 473-487, 'L', 489, 'S', 491-613, 'Y', 615-634,'
A; Cross-references: EMBL:X15332; NID:929545; PIDN:CAA33387.1; PID:9930045
A; Note: the authors' translation of residues 905-932 is inconsistent with the nucleotide R; Seyer, J.M.; Kang, A.H.

A.Accession: S01726
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mrnaslated the codon CAG for residue 154 as His
A.Note: the authors translated the codon CAG for residue 154 as His
A.Moleic A.A.; Ramirez, F.
Nucleic A.A.ids Res. 17, 6742, 1989
A.Fitle: Nucleotide and amino acid sequences of the entire human alpha-1 (III) collagen.
A.Reference number: S04887; MUID:89386015; PMID:2780304

sed - dietord teon	200	probable ATP-bindi	conserved hypothet	tRNA (5-methylamin	anthranilate synth	hypothetical prote	dihydrolipoamide d	NF2d9 - mouse	metalloproteinase	neutral proteinase	hypothetical prote	protein M28.1 [imp	probable homeodoma	probable protein k	low-density lipopr	furin (EC 3.4.21.7
MWOYPON	2000	E83622	AE0095	AI0199	803316	AG1031	A30151	I49257	A47710	140227	T23814	F88297	HB4774	S10932	JE0315	A43434
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1 23	1.00	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1
7	?	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37
ć	2	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1 CGHUTL colladen alpha 1(III) chain precursor - human N)Alternate names: procolladen alpha 1(III) chain C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 24-Apr-1984 #sequence revision 01-Sep-1995 #text_change 21-Jul-2000 C;Date: 24-Apr-1984 #sequence revision 01-Sep-1995 #text_change 21-Jul-2000 C;Acckopi, D.J. Submitted to the EMBL Data Library, February 1989 A;Reference number: S05272 A;Accession: S05272 A;Accession: S05272 A;Actession: System S	A; Molecule type: mRNA A; Molecule type: mRNA A; Cross-references: EMBL:X14420; NID:930057; PIDN:CAA32583.1; PID:930058 A; Cross-references: EMBL:X14420; NID:930057; PIDN:CAA32583.1; PID:930058 B; Ala-Kokko, L.; Kontusaari, S.; Baldwin, C.T.; Kuivaniemi, H.; Prockop, D.J. Biochem. J. 260, 509-516, 1989 A; Title: Structure of cDNA clones coding for the entire prepro-alpha! (III) chain of humar erences. A; Accession: S04642 A; Accession: S04642 A; Molecule type: MRD:89350838; PMID:2764886	A; Cross-references: EMBL:X14420; NID:930057; PIDN:CAA32583.1; PID:930058 A; Cross-references: EMBL:X14420; NID:930057; PIDN:CAA32583.1; PID:930058 A; Note: the complete sequence is not shown R; Benson-Chanda, V.; Su, M.W.; Well, D.; Chu, M.L.; Ramirez, F. Gene 78, 255-265, 1989 A; Title: Cloning and analysis of the 5' portion of the human type-III procollagen gene ((A; Reference number: PE0011; MUID:89378752; PMID:2777083 A; Accession: PE0011 A; Molecule type: DMA	A; Residues: 1-176 & REEN> A; Residues: 1-176 & REEN> A; Cross-references: GB:N26939; NID:9180813; PIDN:AAA52040.1; PID:9180814 R; Toman, P.D.; Ricca, G.A.; de Crombrugghe, B. Nucleic Acids Res. 16, 7201, 1988 A; Title: Nucleotide sequence of a cDNA coding for the amino-terminal region of human pref. A; Reference number: S01726; MUID:88303366; PMID:3405773

Mon Sep

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A; Residues: 950-1018, Y', 1020-1183, S', 1185-1466 cMAN>
A; Residues: 950-1018, Y', 1020-1183, S', 1185-1466 cMAN>
A; Residues: 950-1018, Y', 1020-1183, S', 1185-1466 cMAN>
A; Residues: 950-1018, Y', 1020-1183, S', 1185-1466 cMAN>
A; Accession: 950-1018, A.H.
Biochemistry 20, 2621-2627, 1981
A; Title: Covalent structure of collagen: amino acid sequence of alphal (III)-CB9 from ty)
A; Reference number: A90446; MUID:81208139; PMID:7016180
A; Recession: A90446
A; Residues: 965-979, A', 981-984, 'PS', 987, 'QN', 990-1096, 'P', 1098-1152, 'AT', 1155, 'S', 1157-A; Experimental source: liver
A; Residues: 965-979, A', 981-984, 'PS', 987, 'QN', 990-1096, 'P', 1098-1152, 'AT', 1155, 'S', 1157-A; Experimental source: liver
A; Experimental source: liver
A; Experimental source: liver
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A; Experimental source: liver
A; Residues: 965-979, 'A', 981-984, 'PS', 987, 'QN', 990-1096, 'P', 1088-1152, 'AT', 1155, 'S', 1157-1466 cLOI>
A; Reference number: A93551; MUID:85087944; PMID:6096827
A; Residues: 1065-1155, P', 1157-1466 cLOI>
A; Residues: 1065-1155, P', 1157-1466 cLOI>
A; Residues: 1065-1155, P', 1157-1466 cLOI>
A; Residues: 1065-1155, P', 1157-1466 cLOI>
A; Residues: 1065-1155, P', 1157-1466 cLOI>
A; Residues: 1065-1155, P', 1157-1466 cLOI>
A; Residues: 1065-1155, P', 1157-1466 cLOI>
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A;Residues: 1065-1155, 'P',1157-1466 <LOI>
A;Cross-references: EMBL:X01655; EMBL:X01742; NID:929584; PIDN:CAA25821.1
R;Miskulin, M.; Dalgleish, R.; Kluve-Beckerman, B.; Rennard, S.I.; Tolstoshev, P.; Brant
B;Dchemistry 25, 1408-1413, 1986
A;Title: Human type III collagen gene expression is coordinately modulated with the type
A;Reference number: 152393; MUID:86187804; PMID:3758462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Status: translated from GB/EMBL/DDBJ
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A,Residues: 1176-1240, VV,1242-1356, PV,1358-1466 <CHU>
A,CROSS-references: GB:ML0615, GB:ML0793, GB:ML0794; GB:ML0795, GB:ML0796, GB:ML0797; GB
A,Experimental source: liver
A,Note: the authors translated the codon TTC for residue 1057 as Tyr; the codons given for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit ((
_3-hydroxylated. About 15% of the lysines are 5-hydroxylated and some are subsequently O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: GDB:COL3A1
A;Cross-references: GDB:118729; OMIM:120180
A;Map position: 2q31-2q31
A;Introns: 27/1; 94/3; 11/3; 149/3; 176/3; 554/3; 587/3; 1175/3; 1275/1; 1337/3; 1418/3
A;Introns: 27/1; 94/3; 11/3; 149/3; 176/3; 554/3; 587/3; 1175/3; 1275/1; 1337/3; 1418/3
A;Note: the list of introns is incomplete; defects in this gene can result in Ehlers-Danl C;Complex: type III collagen is a homotrimer of monomers initially linked by disulfide by er of their length, is formed with desmosine cross-links made from lysine and allysine re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Function: structural component of extracellular fibrous polymer that maintains integrords coiled coil, Bilers-Danlos syndrome; extracellular matrix; glycoprotein; byda (5,8uperfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; C; Keywords: coiled coil, Bilers-Danlos syndrome; extracellular matrix; glycoprotein; byda F; 24-123/Domain: signal sequence #status predicted <81G>
F; 24-123/Domain: amino-terminal propeptide #status predicted <PRO>
F; 24-121/Product: collagen alpha 1(III) chain #status predicted <MAT>
F; 154-167/Region: amino-terminal nonhelical telopeptide
F; 168-1196/Region: cell attachment (R-G-D) motif
F; 1197-1221/Region: carboxyl-terminal nonhelical telopeptide
F; 1238-1466/Domain: garboxyl-terminal propeptide #status predicted <CPR>
F; 1238-1466/Domain: fibrillar collagen carboxyl-terminal homology <PCC>
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R;Chu, M.L.; Weil, D.; de Wet, W.; Bernard, M.; Sippola, M.; Ramirez, F.
J. Biol. Chem. 250, 4357-4363, 1985
A;Title: Isolation of cDNA and genomic clones encoding human pro-alphal(III) collagen.
A;Reference number: A92516; MUID:85157600; PMID:2579949
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                                                  A;Status: translation not shown
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A; Residues: 1165-1196 < EMA>
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ARREFERENCE Number: 151868; MUID:93304430; PMID:8317500
ARREFERENCE Number: 151868
ARREFERENCE NUMBER:
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ARREFERENCE NUMBER:
Biochem. J. 311, 332-343, 1335.
ARREFERENCE NUMBER:
ARREFERENCE NUMBER:
ARREFERENCE NUMBER: 559511; MUID:96067614; PMID:7487954
ARREFERENCE NUMBER:
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Biochemistry 16, 1158-1164, 1977

A;Title: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptide
A;Reference number: A30399; MUID:77134724; PMID:557335
A;Residues: "V', 169-225, 229-232, "P', 234-292, "D', 294-398 <SEY1>
A;Residues: "V', 169-225, 229-232, "P', 234-292, "D', 294-398 <SEY1>
A;Residues: "V', 169-225, 229-232, "P', 234-292, "D', 294-398 <SEY1>
A;Residues: acquence corrected by A94562; attachment of 2-O-alpha-D-glucosyl-O-beta-D-galact
R;Seyer, J.M.
submitted to the Atlas, December 1977
A;Reference number: A94562
A;Molecule type: procein
A;Residues: "V', 169-225, 229-277, "A', 279-292, "D', 294, 'S', 296-398 <SEY2>
A;Residues: "V', 169-225, 229-277, "A', 279-292, "D', 294, 'S', 296-398 <SEY2>
A;Residues: "W', 169-225, 229-277, "A', 279-292, "D', 294, 'S', 296-398 <SEY2>
A;Roce: author submitted corrections to A90399
R;Milewicz, D.M.; Witz, A.M.; Smith, A.C.; Manchester, D.K.; Waldstein, G.; Byers, P.H.
Am. J. Hum. Genet. 53, 62-70, 1993
A;Title: Parental somatic and germ-line mosaicism for a multiexon deletion with unusual fspring.
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A;Title: Human pro alpha1(III) collagen: cDNA sequence for the 3'A;Reference number: S02119; MUID:88189827; PMID:3357782
A;Accession: S02119
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Aintrons: 29/1; 95/3; 112/3; 150/3; 175/3; 193/3; 211/3; 229/3; 247/3; 265/3; 283/3; 296/3; 673/3; 706/3; 706/3; 718/3; 756/3; 814/3; 850/3; 868/3; 868/3; 940/3; 976/3; 6.59uperfamily: collagen alpha 1(11) chain, fibrillar collagen carboxyl-terminal homology; C; Keywords: coiled coil; extracellular matrix.

F;1-24/Domain: signal sequence #status predicted <SIG>F;25-154/Domain: propeptide #status predicted <SIG>F;25-154/Domain: von Willebrand factor type C repeat homology <VWC>F;32-92/Domain: von Willebrand factor type C repeat homology <VWC>F;125-1464/Product: collagen alpha 1(III) chain #status predicted <MAT>F;1236-1464/Domain: fibrillar collagen carboxyl-terminal homology <PCC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding two different me
                                                                                                                                                                                                                                                                                                                                                                                                                                        III and IX collagen mRNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable folylpolyglutamate synthase - Mycobacterium tuberculosis (strain H37RV)
C,Species: Mycobacterium tuberculosis
C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Zea mays (maize)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C;Accession: S14999 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
C;Accession: S14997; Mulb: Jan D.B.; Atkinson, B.G.
A;Thle: Sequence, identification and characterization of cDNAs encoding two A;Reference number: S14997; Mulb:91329703; PMID:1714322
                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMEL:X52046; NID:g575321; PIDN:CAA36279.1; PID:g575322 R;Metsaeranta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E. Biochim. Biophys. Acta 1089, 241-243, 1991
A;Title: Specific hybridization probes for mouse type I, II, III and IX col A;Reference number: S16176; MuID:91274355; PMID:2054384
A;Accession: S16373
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A;Residues: 1-161 <GOP>
A;Cross-references: EMBL:X54076; NID:g22338; PIDN:CAA38013.1; PID:g22339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X57983; NID:g50476; PIDN:CAA41048.1; PID:g50477
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Pred. No. 1.6;
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Pred. No. 4.2;
                                                                                                                                                                   submitted to the EMBL Data Library, November 1994 A;Reference number: S62120 A;Accession: S62120
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C;Superfamily: alpha-crystallin
C;Keywords: heat shock; stress-induced protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heat shock protein 18 (clone c9) - maize
                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-866,'G',868-1464 <TOA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.9%;
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                                      A;Molecule type: DNA
A;Residues: 1-1464 <TOM>
A;Cross-references: EMBL:X52046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1203 IAGVGGEKSGG 1213
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Molecule type: DNA
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F70863
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Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 13-Aug-1999
Ciscession: 341067; A29905; 331924
Ridlumoff, V.; Maekelae, J.K.; Vuorio, E.
Bliochim. Biophys. Acta 1217, 41-48, 1994
A; Reference number: S41067 MUD:94114571; PMID:8286415
A; Reference number: S41067
A; Reference number: S41067
A; Reference number: S41067
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A; Reference number: S41067
A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A; Reference number: A29905; MUID:88296083; PMID:2456904
F;24/Wodified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted F;153-154/Cleavage site: Pro-Gln (procollagen N-endopeptidase) #status predicted F;154/Modified site: pyrolidone carboxylic acid (Gln) (in mature form) #status predicted F;161,1212/Modified site: allysine (Lys) #status predicted F;263,284,860,977,1106/Modified site: 5-hydroxylysine (Lys) #status experimental F;263/Binding site: carbohydrate (Lys) (covalent) #status experimental F;584,1094/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental F;948-949/Cleavage site: Gly-11e (collagenase) #status sxperimental F;1106/Binding site: carbohydrate (Lys) (covalent) #status predicted
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Cispecies: Mus musculus (house mouse)
Cjate: 10-Apr-1996 #sequence revision 19-Apr-1996 #text_change 13-Aug-1999
CjAccession: 859856; 862120; 516373
R;Toman, P.D.; de Crombrugghe, B.
R;Toman, P.D.; de Crombrugghe, B.
A;Title: The mouse type-III procollagen-encoding gene: genomic cloning and complete DNA A;Reference number: 859856; MUID:95011609; PMID:7926795
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(Suberfamily: oollagen alpha 1(1) chain, fibrillar collagen carboxyl-terminal homology
C;Reywords: coiled coil, extracellular matrix; glycoprotein; trimer; triple helix
F;408-636/Domain: fibrillar collagen carboxyl-terminal homology <PCC>
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A;Residues: 308-482 <FRA>
A;Residues: GB-482 <FRA>
A;Cross-references: GB-M31354; NID:g203500; PIDN:AAA40942.1; PID:g203501
R;Glumoff, V. Maekelae, J.K.; Vuorio, B.
submitted to the EMBL Data Library, February 1993
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Pred. No. 0.35;
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Pred. No. 0.73;
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ilarity 81.8%;
Conservative
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A;Accession: S31924
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Best Local Similarity
Matches 9; Conserv
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Matches 11; Conserv
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A;Molecule type: mRNA
A;Residues: 2-636 <GL2>
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PBSX prophage ORF xkdo - Bacillus subtilis
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A;Cross-references: GB:299110; GB:AL009126; NID:g2633472; PIDN:CAB13125.1; PID:e1183288;
A;Experimental source: strain 168
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R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; F;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; i. Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N., Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
J. Bacteriol. 179, 7135-7155, 1997
J. Rice, D.; Noelling, J.; Reeve, J.N.
J. Reference number: A69000; MUID:98037514; PMID:9371463
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Assetues: 1-270 cMTH>
Assetues: GB:AE000916; GB:AE000666; NID:g2622674; PIDN:AAB86032.1; PID:g2622686
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                                               A;Residues: 1-209 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK89941.1; PID:g15159896; GSPDB:GN00170
C;Genetics:
A;Gene: AGR L 2749
A;Map position: linear chromosome
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C;Date: 05-Dec_1997 #sequence_revision 05-Dec-1997 #text_change 24-Sep-1999
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Pred. No. 92;
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Pred. No. 11;
1; Mismatches
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Best Local Similarity 72.7%;
Matches 8; Conservative
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Best Local Similarity 70...
7; Conservative
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                      A; Molecule type: DNA
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arylesterase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AE2981
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
R;Wood, D.W.; Setubal, Scant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
Science 294, 2317-232, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Accession: C98302
C;Accession: C98302
C;Accession: B3302
C;Accession: C, Minkle, G,; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Aritle: Genome 294, 233-2328, 2001
A;Aritle: Genome 28quence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A,Reference number: AB2577; MUID:21608550; PMID:11743193

A,Accession: AE2981

A,Status: preliminary
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A;Cross-references: GB:AE008689; PIDN:AAL44267.1; PID:g17741852; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
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Pred. No. 12;
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Best Local Similarity 90.0%;
Matches 9; Conservative
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A; Molecule type: DNA

& g A;Gene: ada

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us-10-615-959-42.rpr

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19.75/2016-rich cell wall protein - carrot (fragment)
C;Species: Daucus carota (carrot)
C;Species: Daucus carota (carrot)
C;Species: Daucus carota (carrot)
C;Species: Daucus carota (carrot)
C;Species: Daucus carota (carrot)
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C;Species: Daucus carota (carota)
C;Species: Daucus carota (carota)
R;Lin, X.; Hwang, G.J.; Zimmerman, J.L.
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Arabidopsis thaliana Gispecies: Arabidopsis thaliana (mouse-ear cress) Gispecies: Arabidopsis thaliana (mouse-ear cress) Gispecies: Arabidopsis thaliana (mouse-ear cress) Gispecies: Arabidopsis thaliana 20-Apr-2000 #text_change 20-Apr-2000 Ciscession: T47394 Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gispecies Gisp
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R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, July 2000
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C,Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
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A;Residues: 1-548 <SCH>
A;Cross-references: EMEL:AL389900; GSPDB:GN00116; NCSP:B15120.50
A;Experimental source: BAC clone B15120; strain OR74A
C;Gene: NCSP:B15120.50
                                                                                                   Length 298;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein B15120.50 [imported] - Neurospora crassa
                                                                                                        5,
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Pred. No. 16;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB 2
Pred. No. 59;
1; Mismatches
                                                                                                                                                                                                   0; Mismatches
                                                                                                        Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.68;
                                                                                                        71.4%;
88.9%;
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Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IAGIGGEKAGG 11
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                                                                                                                                                                                                                                                                                                                                                                              103 AGIGGAKAG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: Z25286
                                                                                                                                                                                                                                                                                        2 AGIGGEKAG 10
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                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: T51035
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 6
                   A, Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
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A;Status: preliminary
A;Residues: 1-298 «KUR»
A;Rolecule type: DNA
A;Residues: 1-298 «KUR»
A;Rolecule type: DNA
A;Residues: 1-298 «KUR»
A;Rolecule type: DNA
A;Residues: 1-298 «KUR»
A;Rolecule type: DNA
A;Residues: 1-298 «KUR»
B;Galibert, F: Finan, T:M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, P;Galibert, F.; Finan, T:M.; Jones, T
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure, A;Atthors: Kahn, D.; Kahn, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Acterence number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Species: Methanobacterium thermoautotrophicum
C.Species: U-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 20-Jun-2000
C.Accession: 851346, 857457
R.Hochheimer, A.; Schmitz, R.A.; Thauer, R.K.; Hedderich, R.
R.Hochheimer, A.; Schmitz, R.A.; Thauer, R.K.; Hedderich, R.
A.Title: The tungsten formylmethanofuran dehydrogenase from Methanobacterium thermoautot
A.Reference number: 863519; MUID:96163477; PMID:8575452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Complex: heterotetramer of A (see PIR:S57456), B (see PIR:S57458), C, and D (see PIR:G
C;Superfamily: formylmethanofuran dehydrogenase chain C
C;Keywords: heterotetramer; iron-sulfur protein; metalloprotein; oxidoreductase; tungste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein SMa0367 [imported] - Sinorhizobium meliloti (strain 1021) magaplasm C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: E55286
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows r; Ralman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883, 2001
A;Title: Mucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             formylmethanofuran dehydrogenase (EC 1.2.99.5) (tungsten) chain C - Methanobacterium the
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A;Experimental source: strain Marburg, DSM 2133
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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0
                                                                                               A,Gene: MTH1558
C,Superfamily: formylmethanofuran dehydrogenase chain C
C,Keywords: iron-sulfur protein; metalloprotein; oxidoreductase;
                                                                                                                                                                                                                                                                                   Score 40; DB 2; Length 270;
Pred. No. 31;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.4%; Score 40; DB 2; Length 270; 63.6%; Pred. No. 31; ive 2; Mismatches 2; Indels
A,Experimental source: strain Delta H
C,Genetics:
                                                                                                                                                                                                                                                                                        71.4%;
ilarity 63.6%;
Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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197 VARVGGEMAGG 207
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197 VARVGGEMAGG 207
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Best Local Similarity '
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A;Molecule type: DNA
A;Residues: 1-270 <HOC>
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submitted to the Protein Sequence Database, March 2000

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Atternate names: homeotic protein MAB66

N;Alternate names: homeotic protein MAB66

C;Becise: Mus musculus (house mouse)

C;Becise: Mus musculus (house mouse)

C;Accession: 149754; F37290; B4160; F38809

C;Accession: 149754; F37290; B4160; F38809

C;Accession: 149754; F37290; B4160; F38809

C;Accession: 149754; F37290; B4160; F38809

R;Benson, G.V.; Nguyen, T.H.; Maas, R.L.

Mol. Cell. Biol. 15, 1591-1601, 1995

A;Attle: The expression pattern of the murine Hoxa-10 gene and the sequence recognition
A;Reference number: 149754; MUID:95166244; PMID:7862151

A;Accession: 149754

A;Accuse references GB:L08757; NID:9825647; PIDN:AAA67125.1; PID:9567213

A;Ascession: R37290; MUID:92073356; PMID:1683707

A;Accession: F37290

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A; Residues: 325-384 <SIN>
R; Mutcha, M.T.; Leckman, J.F.; Ruddle, F.H.
Proc. Natl. Acad. Sci. U.S.A. 88, 10711-10715, 1991
A; Rittle: Detection of homeobox genes in development and evolution.
A; Reference number: A41606; MUID:92073357; PMID:1720547
A; Rocession: B41606
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 346-370 <MUR>
A; Ross-references: GB:MB1659; NID:g193973; PIDN:AAA63312.1; PID:g193974
C; Genetics:
A; Greetics:
A; Greetics:
C; Superfamily: unassigned homeobox proteins; homeobox homology
C; Keywords: DNA binding; homeobox; nucleus; transcription regulation
F; 326-382/Domain: homeobox homology <ANOX>
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                 69.6%; Score 39; DB 2; Length 163; 77.8%; Pred. No. 28; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.6%; Score 39; DB 2; Length 399; 70.0%; Pred. No. 64; tive 1; Mismatches 2; Indels
A,Reference number: 224464
A,Accession: T47394
A,Status: preliminary
A,Molecule type: DNA
A,Rebidus: 1-163 <MAS>
A,Crose-references: EMBL:AL138644
A,Experimental source: cultivar Columbia; BAC clone T18D12
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Best Local Similarity 70.00
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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99 GIGGDKFGG 107
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A; Introns: 150/1
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Search completed: September 18, 2004, 04:30:53 Job time: 15.3725 secs

||:|| AGVGGGSAGG 34 us-10-615-959-42.rsp

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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 18, 2004, 03:48:54; Search time 8.19608 Seconds (without alignments) 69.884 Million cell updates/sec Run on:

US-10-615-959-42 56 1 IAGIGGEKAGG 11 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched: 141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Description	P02461 homo sapien	P13941 rattus norv	1 mus	н	٠.	027600 methanobact	Q59579 methanobact	P08675 plasmodium	0	N	н	a	_			P05378 thermus the		Q00891 bacillus me	6		Q8xv18 ralstonia s	074031 methanobact		Q8ker7 chlorobium			P39371 escherichia		-	P36591 schizosacch		drosoph	P08543 herpes simp
ID	CA13 HUMAN	CA13 RAT	CA13_MOUSE	HS21 MAIZE	XKDO BACSU	FWDC METTH	FWDC MET'TM	CSP PLACL	HXAA MOUSE	FUR2_DROME	TBX2_CAEEL	AMPA PSEAE	POLG PWVMI	RF1 LEPIN	TRMU YERPE	TRPE THETH	DLDH_YEAST	NPRM BACME	CORI MOUSE	YDL8 SCHPO	RS3 RALSO	FWDC METWO	FMDC_METBA	ILVC CHLTE	ILVC_THETN	FL3H_DIACA	YJHT ECOLI	RPA2 METVA	MB48 MYCTU	DYR SCHPO	HS70 PARBR	SGG DROME	RIRI HSV11
Query Match Length DB	1466 1	636 1	1464 1	161 1	1332 1	270 1	270 1	378 1	399 1	1679 1	423 1	495 1	269 1	354 1	371 1	462 1	499 I	562 1	1113 1	214 1	264 1	270 1	301 1	330 1	331 1	365 1	368 1	386 1	460 1	461 1	649 1	1067 1	1137 1
Query Match I	100.0	92.9	92.9	78.6	73.2	71.4	71.4	9.69	9.69	9.69	67.9	67.9	66.1	66.1	66.1	66.1	66.1	66.1	66.1	64.3	64.3	64.3	64.3	64.3	64.3	64.3	64.3	64.3	64.3	64.3	64.3	64.3	64.3
Score	56	52	52	44	41	40	40	39	39	39	38	38	37	37	37	37	37	37	37	36	36	36	36	36	36	36	36	36	36	36	36	36	36
Result No.		8	3	4	υ	φ	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

076743 caenorhabdi Q9v110 pyrococcus	059229 pyrococcus P29161 thermococcu	Q9hih6 thermoplasm Q8drs4 streptococc	P48619 ricinus com P94188 alcaligenes	Q54970 streptococc Q92804 homo sapien	08zzj7 pyrobaculum
GLH4_CAEEL RS12_PYRAB	RS12_PYRHO RS12_THECE	VHB CRAPE YD63 THEAC TRMU STRMU	FD3C_RICCO MERA_ALCSP	POXB_STRPN RB56_HUMAN	PURL_PYRAE
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1156	147	312 312 373	460 559	591 592	697
64.3	623.5	62.5	62.5	62.5 62.5	62.5
36	) M M (	 	35	35 35	32
34	36	w w 4 w w 0	42	43 44	45

# ALIGNMENTS

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us-10-615-959-42.rsp

[19] Chu M.-L., Weil D., de Wet W.J., Bernard M.P., Sippola M., Ramirez F., "Isolation of cDNA and genomic clones encoding human pro-alpha 1 (III) collagen. Partial characterization of the 3' end region of the SEQUENCE OF 1065-1466 FROM N.A.
MEDLINE-BS097944; PubMed=6096827;
Loidl H.R., Brinker J.M., May M., Pihlajaniemi T., Morxow S.,
Rosenbloom J., Myers J.C.;
"Molecular cloning and carboxyl-propeptide analysis of human type III Kuivaniemi H., Tromp G., Prockop D.J.;
"Mutations in fibrilar collagens (types I, II, III, and XI), fibrilassociated collagen (type IX), and network-forming collagen (type X)
cause a spectrum of diseases of bone, cartilage, and blood vessels."; Toman D., Ricca G., de Crombrugghe B., "Nucleotide sequence of a cDNA coding for the amino-terminal region of human prepro alpha 1(III) collagen.", Nucleic Acids Res. 16:7201-7201(1988). VARÍANT AORTIC ANBURYSM ARG-303, AND VARIANT THR-668.
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Tromp G., Wu Y., Prockop D.J., Madhatheri S.L., Kleinert C.,
Earley J.J., Zhuang J., Noerrgaard O., Darling R.C., Abbott W.M.,
Cole C.W., Jaakkola P., Rynaenen M., Pearce W.H., Yao J.S.T.,
Majamaa K., Smullens S.N., Gatalica Z., Ferrell R.E., Jimenez S.A., MEDLINE=86187804; PubMed=3754462; Miskulin M., Dalgleish R., Kluve-Beckerman B., Rennard S.I., Tolstoshev P., Brantly M., Crystal R.G.; "Human type III collagen gene expression is coordinately modulated with the type I collagen genes during fibroblast growth."; Biochemistry 25:1408-1413(1986). SEQUENCE OF 950-1466 FROM N.A.
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Mankoo B.S., Dalgleish R.;
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Benson-Chanda V., Su M.W., Weil D., Chu M.-L., Ramirez F.;
"Cloning and analysis of the 5' portion of the human type-III
Gene 78:255-265(1989). Nucleic Acids Res. 16:11833-11833(1988), 18 Nucleic Acids Res. 12:9383-9394 (1984) Biol. Chem. 260:4357-4363(1985). Molyneux K., Dalgleish R.; "Human type III collagen 'variant' SEQUENCE OF 1176-1466 FROM N.A. MEDLINE=85157600; PubMed=2579949; REVISION TO 1184, MEDLINE=89098346; PubMed=3211760; SEQUENCE OF 1-170 FROM N.A. TISSUE=Placenta; MEDLINE=88303360; PubMed=3405773; MEDLINE=97255959; PubMed=9101290; SEQUENCE OF 1161-1200 FROM N.A. Hum. Mutat. 9:300-315(1997). SEQUENCE OF 965-1200 REVIEW ON VARIANTS. procollagen." 

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MEDLINE=95268429; PubMed=7749417;
Tromp G., de Paepe A., Nuytinck L., Madhatheri S.L., Kuivaniemi Substitution of valine for glycine 793 in type III procollagen Ehlers-Danlos syndrome type IV.";
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                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                               Gaps
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=9414571; PubMed=8286415;
MEDLINE=9414571; PubMed=8286415;
Glumoff V., Maekelae J.K., Vuorio B.;
"Cloning of cDNA for rat pro alpha 1(III) collagen mRNA. Different expression patterns of type I and type III collagen and fibronectin experssion patterns of type I and type III collagen and fibronectin Biochim. Biophys. Acta 1217:41-48(1994).
                               ..
0
100.0%; Score 56; DB 1; Length 1466; 100.0%; Pred. No. 0.21; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Sprague-Dawley; TISSUB=Fibroblast,
Wurtz T., Ellerstroem C., Lundmark C., Christersson C.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                  PISST. 070664; PRT; 636 AA. 01-34N-1990 (Rel. 13, Created) 01-JUN-1994 (Rel. 29, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Collagen alpha 1(III) chain (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR00816; Clg helix.
InterPro; IPR008160; Collagen.
InterPro; IPR00160; Fib_collagen_C.
InterPro; IPR00181; Fib_collagen_C.
InterPro; IPR001007; VWFC.
Pfan; PF01491; CoLFT; 1.
Pfan; PF01491; Collagen; 6.
ProDom; PD000007; Clg helix; 1.
ProDom; PD002078; Fib_collagen_C; 1.
                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ005395; CAA06510.1; -. EMBL; M21354; AAA40942.1; -. PIR; S41067; S41067.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 73-636 FROM N.A.
                                                                                           1205 IAGIGGEKAGG 1215
                                 11; Conservative
                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                             1 IAGIGGEKAGG 11
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                 NCBI TaxID=10116;
                               Matches
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SETAIN=C57BL/6; ITSSUE=Brain;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Itschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Worley K.C., Hale S., Garrinci P., Prange C.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raber J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N. Krzywinski M.I., Skalska U., Smailus D.E.,

Raber T., Boneration and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CS'BL/6 X DBA; TISSUE=Embryo;
MEDLINE=95011609; PubMed=7926795;
Toman D., de Crombrugghe B.;
Tyle mouse type-III procollagen-encoding gene: genomic cloning and complete DNA sequence.";
Gene 147:161-168(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
   PROSITE; PS01208; VWPC 1; PARTIAL.

Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
Collagen; Glycoprotein.

NON TER 1 1 1 CHAIN CHAIN CHAIN 376 636 CARBOXYL-TERMINAL PROPERTIDE.
                                                                                                                                                                                                                                                                             .
                                                                     COLLAGEN ALPHA 1(III) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE.
TRIPLE-HELICAL REGION (C-TERMINAL).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                           Length 636;
                                                                                                                                     INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N -> D (IN REF. 2).
A -> G (IN REF. 2).
                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                            61A48159F01D01EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                              Score 52; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                              CA13 MOUSE STANDARD; PRT; 1464 AA. P08121; Q61429; Q9CRN7; Created) 15-UU-1988 (Rel. 08, Created) 15-UU-199 (Rel. 38, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Collagen alpha 1(III) chain precursor.
                                                                                                                                                                                                                                                            Pred. No. 0.43;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88167858; PubMed=3443309; Wood L., Theriault N., Vogeli G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human and mouse cDNA sequences.
                                                                                                                                                                                                               62332 MW;
                                                                                                                                                                                                                                              92.9%;
81.8%;
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                                                                                                                                                                                                                             Query Match
Best Local Similarity 81...
9; Conservative
SMART; SM00038; COLFI; 1.
                                                                                                                                                                                                                                                                                                                                               375 IAGVGGEKSGG 385
                                                                                                                                                                                                                                                                                                                1 IAGIGGEKAGG 11
                                                                            375
636
636
3368
340
340
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                                                                                                                                             368
369
340
340
429
636 AA;
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                                                                                                                                               DISULFID
                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                 SEQUENCE
                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                    CA13_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
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Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa M., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ruell P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackehusa H., Schiml E., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackehusa J., Schiml P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackehusa J., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Whitsher C., Whittaker C., Wilming L., Whishbay-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochim. Biophys. Acta 1089:241-243(1991).

-1-FUNCTION: Collagen type III occurs in most soft connective tissues along with type I collagen.

-1-SUBUNIT: Trimers of identical alpha 1(III) chains. The chains are linked to each other by interchain disulfide bonds. Trimers are also cross-linked via hydroxylysines.

-1-FTM: Proline residues at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the
    the N-terminal domains of the murine
                                                                          SEQUENCE OF 1-28 FROM N.A.
MEDLINE=85131189; PubMed=3972847;
Liau G., Mudryj M., de Crombrugghe B.;
"Identification of the promoter and first exon of the mouse alpha 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Metsaeranta M., Toman D., de Crombrugghe B., Vuorio B., "Specific hybridization probes for mouse type I, II, III and IX
                                                                                                                                                                                                            SEQUENCE OF 810-1464 FROM N.A.
STRAIN=C57BL/6J; TISSUE=Embryonic head;
MEDLINE=21085660; Pubmed=11217851;
"Complete nucleotide sequence of that
alpha-1 type-III collagen chain.";
Gene 61:225-230(1987).
                                                                                                                                                      (III) collagen gene.";
J. Biol. Chem. 260:3773-3777(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91274355; PubMed=2054384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1442-1464 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              collagen mRNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6;
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-!- SIMITARITY: PLANTS HAVE FOUR CLASSES OF HSP20: CLASS I AND II WHICH ARE CYTOPLASMIC; CLASS III WHICH IS IN THE CHLOROPLAST AND CLASS IV WHICH IS IN THE ENDOMEMBRANE. THIS PROTEIN BELONGS
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=cv. Ohio 41; TISSUE=Radicle;
MEDLINE=91329703; PubMed=1714322;
MEDLINE=91329703; PubMed=1714322;
GODING I.S., Frappler J.R.H., Walden D.B., Atkinson B.G.;
"Sequence, identification and characterization of cDNAs encoding tw different members of the 18 kDa heat shock family of Zea mays L.";
Plant Mol. Biol. 16:699-11(1991).
-I. SUBCELLUAR LOCATION: Cytoplasmic.
-I. SUBCELLUAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                          01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-JWD-1994 (Rel. 29, Last annotation update)
17.5 kDa class II heat shock protein.
Zea mays (Maize).
                                                                                                                                                                                               161 AA
                                                                                                                                                                                               PRT;
                                                                                                   |||:||||:||
1203 IAGVGGEKSGG 1213
                                                                                                                                                                                               STANDARD;
                                                                                1 IAGIGGEKAGG 11
NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TO CLASS II.
                                                                                                                                                                                               HS21 MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family
                                                                                                                                                                                                             P24631;
                                                                                                                                                                 JT 4
MAIZE
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EMBL; X52046; CAA36279.1; -.
EMBL; BC043089; AAH43089.1; -.
EMBL; BC08724; AAH53724.1; -.
EMBL; M18933; AAA7738.1; -.
EMBL; K03037; -; NOT ANNOTATED CDS.
EMBL; X57983; CAA41048.1; -.
PIR; A77353; A27353.
PIR; S58856; S59856.
MGD; MGI:88453; CO13a1.

PTM: 0-linked glycan consists of a Glc-Gal disaccharide bound to the oxygen atom of a post-translationally added hydroxyl group (By

chains.

similarity).
SIMILARITY: Contains 1 VWFC domain.

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Gaps

; 0

0; Indels

Length 1464;

Score 52; DB 1;

92.9%; 81.8%;

Pred. No. 0.92;

2; Mismatches

Conservative

NONHELICAL REGION (C-TERMINAL).

O-LINKED (GAL. . ) (BY SIMILARITY).

HYDROXYLATION (BY SIMILARITY).

HYDROXYLATION (BY SIMILARITY).

HYDROXYLATION (BY SIMILARITY).

HYDROXYLATION (BY SIMILARITY).

HYDROXYLATION (BY SIMILARITY).

HYDROXYLATION (BY SIMILARITY).

INTERCHAIN (BY SIMILARITY).

INTERCHAIN (BY SIMILARITY).

HYDROXYLATION (BY SIMILARITY 976 976 HYDROXYLATION (BY SIMILARITY) 11093 HYDROXYLATION (BY SIMILARITY) 1105 1105 HYDROXYLATION (BY SIMILARITY) 11195 1196 INTERCHAIN (BY SIMILARITY) 1196 1196 INTERCHAIN (BY SIMILARITY) 1464 AA; 138944 MW; 2104EC27A886090B CRC64;

MOD\_RES DISULFID

MOD\_RES MOD\_RES

RES

Q Q

DISULFID SEQUENCE

CARBOHYD

DOMAIN

DOMAIN

MOD RES

PROSITE; PS01208; VWFC\_1; 1. PROSITE; PS50184; VWFC\_2; 1. Extracellular matrix; Connective tissue; Repeat; Hydroxylation;

Collagen; Signal

3lycoprotein;

CHAIN PROPEP DOMAIN

PROPEP

InterProj IPR001007; VWF\_C.
PEAG, PF01410; COLF!, 1.
PEAM, PF01491; COLFI, 1.
ProDom; PD000007; Clg\_helix; 1.
ProDom; PD000078; Fib\_collagen\_C; 1.
SWART; SW00038; COLFI\_1.
SWART; SW00214; VWC; 1.

InterPro; IPR008160; Collagen. InterPro; IPR000885; Fib\_collagen\_C. InterPro; IPR002181; Fibrinogen\_C.

InterPro; IPR008161; Clg helix. InterPro; IPR008160; Collagen.

BY SIMILARITY.

BY SIMILARITY.

AMINO-TERMINAL PROPEPTIDE.

COLLAGEN ALPHA 1(111) CHAIN.

CARBOXYL-TERMINAL PROPEPTIDE.

WRC.

WORLELICAL REGION (N-TERMINAL).

TRIPLE-HELICAL REGION.

NONHELICAL REGION (C-TERMINAL).

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A MEDINE-19044035, Tubmed-190435, A MEDINE-19044035, Tubmed-19044035, Tubmed-19044035, Tubmed-19044035, Tubmed-19044035, Tubmed-19044035, Tubmed-19044035, Tubmed-19044035, Tubmed-19046, Tubmed-19046, Tubmed-19046, Tubmed-19046, Tubmed-19046, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-1904, Tubmed-190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78.6%; Score 44; DB 1; Length 161; 80.0%; Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Krogh S., O'Reilly M., Nolan N., Devine K.M.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00011; HSP20; 1.
PROSITE; PS01031; HSP20; 1.
Heat shock; Multigene family.
SEQUENCE 161 AA; 17511 MW; 3E60A8DD4396577C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0cT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
110-0CT-2003 (Rel. 42, Last annotation update)
Phage-like element PBSX protein xkdo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1332 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002068; HSp20.
InterPro; IPR008978; HSP20_chap.
                                                                                                                                                                                                                                                                               EMBL; X54076; CAA38013.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AGIGGEKAGG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 AGAGGDKAGG 36
                                                                                                                                                                                                                                                                                                                    PIR; S14998; S14998.
MaizeDB; 51309; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKDO OR BSU12680.
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XKDO_BACSU
TD _XKDO_BACSU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=9837514; PubMed=9371463;

MEDLINE=9837514; PubMed=9371463;

Andredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

Andredge T., Bashirzadeh P., Lumm W., Pothier B., Qiu D.,

Andredge T., Meang L., Keagle P., Lumm W., Pothier B., Qiu D.,

Andredge T., Mang Y., Wierzbowski J., Gibson R.,

Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,

McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

"Complete genome sequence of Methanobacterium thermoautotrophicum
"Complete genome sequence of Methanobacterium thermoautotrophicum
"T. Bacteriol. 179:7135-7155 (1997).

"Bacteriol. 179:7135-7155 (1997).

"ENGRING CATALYZES THE REVERSIBLE OXIDATION OF CO(2) AND

METHANOPURAN (MRR) TO N-PORMYLMETHANOFURAN (CHO-MFR). CAN ONLY

OXIDISE FORMYLMETHANOFURAN. THIS ENZYME IS OXYCEN-LABILE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- COFACTOR: Tungsten.
-!- ENZYME REGULATION: Not inactivated by cyanide.
-!- ENZYME REGULATION: Not inactivated by cyanide.
-!- PATHWAY: Methanogenesis; first step.
-!- SUBUNIT: THIS ENZYME IS COMPOSED OF SEVEN SUBUNITS FWDA (65 kDa), FWDE (53 kDa), FWDC (31 kDa), FWDD (15 kDa), FWDE, FWDC.
-!- INDUCTION: By growth on tungsten or molybdenum under anaerobic
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- CATALYTIC ACTIVITY: Formylmethanofuran + H(2)O + acceptor = CO(2) + methanofuran + reduced acceptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-NAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tungsten-containing formylmethanofuran dehydrogenase II subunit (BC 1.2.99.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.2%; Score 41; DB 1; Length 1332; 70.0%; Pred. No. 51; 1; Indels cive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1332 AA; 145149 MW; A96C9C9F9E31DF01 CRC64;
                                                                                                        Nature 390:249-256(1997).
-!- SIMILARITY: STRONG, TO B.SUBTILIS YQBO.
                                                                                                                                                                                                                                                                                                                                                     EMBL; Z70177; CAA94037.1; -.
EMBL; Z99110; CAB13125.1; -.
PIR; F69722; F66732.
Subtilist; BG11549; xkdo.
InterPro; IPR008258; SLT_dom.
Pfam; PF01464; SLT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last seq.
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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469 VGGIGGEEAG 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome
SEQUENCE 1332 A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FWDC METTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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FWDC_METTH
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                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COFACTOR: Tungsten.
PATHWAX: Methanogenesis; first step.
SUBUNIT: THIS ENZYME IS COMPOSED OF SEVEN SUBUNITS FWDA (65 kDa),
FWDB (53 kDa), FWDC (31 kDa), FWDD (15 kDa), FWDE, AND FWDG
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                         Complete proteome [GW] -X-X-M-X-X-G-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDUCTION: By growth on tungsten or molybdenum under anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Tungsten-containing formylmethanofuran dehydrogenase II subunit (EC 1.2.99.5).
                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                    Score 40; DB 1; Length 270;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                              043A9FFBBA554D36 CRC64;
                                                                                                                                                                     Oxidoreductase; Tungsten; Methanogenesis; Repeat;

DOMAIN 80 213 7 X 13 AA REPEATS OF

X-[IL]-X-[IV]-X-G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conditions. SIMILARITY: Belongs to the fwdC/fmdC family.
SIMILARITY: Belongs to the fwdC/fmdC family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 AA
                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      + methanofuran + reduced acceptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                    EMBL; AE000916; AAB86032.1; -.
PIR; H69074; H69074.
InterPro; IPR002489; DUF14.
                                                                                                                                                                                                                                                                                              28641 MW;
                                                                                                                                                                                                                                                                                                                     71.4%;
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 63.00,
Best Accordance 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   :| :||| |||
VARVGGEMAGG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                          Pfam; PF01493; GXGXG; 1
                                                                                                                                                                                                                                                                                                                                                                      1 IAGIGGEKAGG 11
                                                                                                                                                                                                                                                                                             270 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=79929;
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99
118
144
163
182
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Q59579; 008493;
30-MAY-2000 (Rel
                                                                                                                                                                                                                                                                                                                                                                                             197
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REPEAT
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   restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -I- MISCELLANEOUS: The circumsporozoite protein is the immunodominant surface antigen on the sporozoite (the infective stage of the malaria parasite that is transmitted from the mosquito to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- MISCELLANEOUS: The C-terminal region is probably used for anchoring the protein to the cell membrane. The repeat sequences would be the surface antigen of the organism.
-!- SIMILARITY: Contains 1 TSP type-1 domain.
                                                                                                                                                                                                                                                                                                [GW] -X-X-M-X-X-G-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=87102878; PubMed=3802196;
Galinski M.R., Arnot D.E., Cochrane A.H., Barnwell J.W.,
Nussenzweig R.S., Enea V.;
"The circumsporozoite gene of the Plasmodium cynomolgi complex.";
Cell 48:311-319(1987).
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15-WAR-2004 (Rel. 43, Last annotation update)
Circumsporozoite protein precursor (CS).
Plasmodium cynomolgi (strain London).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E0A369D2ACFEC46F CRC64;
There are no
                                                                                                                                                                          EMBL; X87970; CAMBLILL.,
InterPro; IPR007489; DUF14,
Ifam; PF01493; GXGKG; 1.
Oxidoreductase; Tungsten; Methanogenesis; Repeat.
DOMAIN 80 213 7 X 13 AA REPEATS OF
X-[IL]-X-[IV]-X-G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 1;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         378 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
European Bioinformatics Institute.
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PRINTS; PR0130; CRCMSPRZOITE.
SMART, SM00209; TSP1; 1.
PROSITE; PS50022; TSP1, 1.
Malaria; Sporozoite; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003067; Crcmsprzoite. InterPro; IPR000884; TSP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28554 MW;
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197 VARVGGEMAGG 207
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270 AA;
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118
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CSP_PLACL
AC P08675;
DT 01.JAN-1988
DT 01.JAN-1988
DT 15-MAR-2004
DE Circumsporo
OS Plaarmodium
OC EUKATYOTA;
OX NEBLINE-871
RA GALINSKi M.
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STRAIN=C57BL/6; TISSUE=Spleen;
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ID FURZ DROME
AC P30432; Q24301;
                                                                                                                                                                          Name=1
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DNA_BIND
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MEDLINE=59166244; PubMed=7862151;
MEDLINE=59166244; PubMed=7862151;
Benson G.V., Nguyen T.-H.E., Maas R.L.;
"The expression pattern of the murine Hoxa-10 gene and the sequence recognition of its homeodomain reveal specific properties of Abdominal B-like genes.",
Mol. Cell. Biol. 15:1591-1601(1995).
                CIRCUMSPOROZOITE PROTEIN.
18 X 6 AA TANDEM REPEATS OF D-G-A-R-A-
                                                                                                                                                                                                                                                                                          1-17.
1-18.
6 X 11 AA TANDEM REPEATS OF G-N-[QR]-
[AE]-G-G-Q-A-G-A-G.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
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MEDLINE=92073356; PubMed=1683707;
Singh G., Kaur S., Stock J.L., Jenkins N.A., Gilbert D.J.,
Copeland N.G., Potter S.S.;
"Identification of 10 murine homeobox genes.";
Proc. Natl. Acad. Sci. U.S.A. 88:10706-10710(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 1; Length 378;
Pred. No. 34;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      SP TYPE-1.
8295A913C36420C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993 (Rel. 26, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
 PROBABLE
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HOXA10 OR HOXA-10 OR HOX-1.8
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1116
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1122
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234
245
256
267
304
378 AA;
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nes 7; Conserv
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                                                         HXAA MOUSE
P31310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                  CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                         ISOGG=P11310-2; Sequence=VSP 002386, VSP 002387; ISSUE SPECIFICITY: EXPRESSED IN THE DEVELOPING LIMB BUD WHERE IT RESCRIFTED TO THE MESENCHYME ALONG THE PROXIMAL-DISTAL AXIS. ALSO FOUND IN DEVELOPING GUT AND UNCGENITAL TRACT. IN ADULT TISSUE, BOTH FORMS FOUND IN KIDNEY BUT ONLY ISOFORM I IS EXPRESSED
MEDINE=92073357; PubMed=1720547;
Murtha M.T., Leckman J.F., Ruddle F.H.;
Murtha M.T., Leckman J.F., Ruddle F.H.;
Murtha M.T., Leckman J.F., Ruddle F.H.;
Murtha M.T., Leckman J.F., Ruddle F.H.;
Proc. Natl. Acad. Sci. U.S.A. 88:10711-10715(1991).
-!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH SPECIFIC POSITIONAL IDENTITIES ON THE ANYERIOR-POSIFERIOR AXIS.
BINDS TO THE DNA SEQUENCE 5'-AA[AT]TTTATTAC-3'.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- DEVELOPMENTAL STAGE: EMBRYONIC EXPRESSION INCREASES FROM DAY 9 TO DAY 12 AND THEN DECLINES TO DAY 15.
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InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
PRINTS; PR00024; HOMEOBOX.
ProDom; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS00027; HOMEOBOX 2; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein;
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Pred. No. 36;
1; Mismatches 2; Indels
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DSL -> MCQ (in isoform 2).
/FTId=VSP 002387.
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26 38 GLY-RICH.

DOMAIN 77 90 POLY-GLY.

POLY-GLY.

DOMAIN 113 144 GLN/PRO-RICH.

DOMAIN 215 222 POLY-GLY.
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EMBL; M81659; AAA63312.1; -.
PIR; 149754; 149754.
HSSP; PO2833; 9ANT.
TRANSFAC; T01715; -.
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REDILINE-2019606 PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

RA Adams M.D., Celniker S.E., Richards S. M., Hoskins R.A., Galle R.F.,

RA Button R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Man K.H., Doyle C., Baxer E.G., Helf G., Nelson C.R., Miklos G.L.G.,

BATIL M. R., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Cawley S., Dolhke C., Broketen P., Brottier P.,

RA Ballew R.M., Cawley S., Dalhke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dalhke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dalhke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dalhke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dalke C., Bavenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Mannes M., Dugan-Rocha S., Pleiter B.C.,

RA Cherry J.M., Cawley S., Heiman T.J., Hernandez J.R. Houck J.,

RA Glodek A., Gong F., Gortell J.H., Gu Z., Galan P., Harris M.,

RA Lish R., Harvey D.A., Heiman T.J., Wei M.-H., Harris M.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Rulp D., Lai Z.,

Lasko P., Lei Y., Leviteky A.A., Li J.H., Li Z., Liang Y., Lin X.,

RA Rimmel B.E., Kodira C.D., Kraft C., Kravitz S., Rulp D., Lai Z.,

RA Martel B.E., Mointon M., Wurphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Oregon-R, Tuebingen, and Iso-1; MRDLLHR=92381036; PubMed=1512259; MRDLLHR=923810136; PubMed=1512259; Roebroek A.J.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dumke U., Rentrop M., Gateff E.A.F., Leunissen J.A.M., van de Ven W.J.M.; "Cloning and functional expression of Dfurin2, a subtilisin-like proprotein processing enzyme of Drosophila melanogaster with multiple repeats of a cysteine motif.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The Dfurz gene of Drosophila melanogaster: genetic organization, expression during embryogenesis, and pro-protein processing activity of its translational product Dfurin2.";

DNA Cell Biol. 14:223-234(1995).
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MEDIJIRE=95186060; PubMed=7880443;
ROEDTOER A.J.M., Ayoubi T.A.Y., Creemers J.W.M., Pauli I.G.L., van de Ven W.J.M.;
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
01-APR-1993 (Rel. 25, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Furin-like procease 2 precursor (EC 3.4.21.75) (Furin 2).
FUR2 OR CG18734/CG4235.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 267:17208-17215(1992),
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activity within constitutive secretory pathways and capable of cleavage at the RX(K/R)R consensus motif (By similarity).
CATALYTIC ACTIVITY: Release of mature proteins from their proproteins by cleavage of Arg-Kaa-Yaa-Arg-|-Zaa bonds, where Xaa can be any amino acid and Yaa is Arg or Lys. Releases albumin, complement component C3 and von Willebrand factor from their
                                                                                                        Expression
                                                                           respective precursors.

TISSUE SPECIFICITY: Transient expression in a subset of central nervous system neurons during embryonic stages 12-13. Expression in developing tracheal tree from stage 13 to end of embryonic
                                                                                                                                            DEVELOPMENTAL STAGE: Expressed both maternally and zygotically. SIMILARITY: Belongs to peptidase family S8. Furin subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00156; SUBTILASE ASP; 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00137; SUBTILASE ENS; 1.
Hydrolase; Serine protease; Glycoprotein; Signal; Transmembrane; Multigene family; Zymogen; Repeat.
SIGNAL 1
PROPEP ? 318
POTENTIAL.
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GO; GO:0004276; F:furin activity; IDA.
InterPro; IPR006512; Furin repeat.
InterPro; IPR003093; Grow Fac recep.
InterPro; IPR00209; Peptidase_S8.
InterPro; IPR002084; Peptidase_S8B.
InterPro; IPR003084; Peptidase_S8B.
InterPro; IPR003084; Peptidase_S8B.
Ffam; PF00483; P. Proprotein; Z.
Pfam; PF00082; Peptidase_S8; 1.
PRNINTS; PR00723; SUBTILISIN.
SNART; SM00261; FU; 10.
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EMBL; L33831; AAA69860.1; -.
EMBL; AE003502; AAF48598.1; -.
PIR; A43434; A43434.
HSSP; Q99405; 1MPT.
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CARBOHYD

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NCBI_TaxID=287;
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                               AMPA_PSEAE
  RESULT 12
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Rhabditidae, Peloderinae, Caenorhabditis.
     (POTENTIAL). (POTENTIAL).
                                                        (POTENTIAL).
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1274 1274 N-LINKED (GLCNAC. . .) (FOLES 1277 1277 N-LINKED (GLCNAC. . .) (POTE 1439 N-LINKED (GLCNAC. . .) (POTE 152 153 MLSSING (IN REF. 1). (POTE 177 177 V -> P (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 1873 213 V -> VDQL (IN REF. 1). (POTE 18
                                                                                                                                                                                                                                              Pred. No. 1.3e+02;
3; Mismatches 1; Indels
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-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: Contains 1 T-box domain.
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PROSITE; PS01264; TBOX 2; 1.
PROSITE; PS0252; TSOX 3; 1.
Hypothetical protein; DNA-binding; Nuclear protein.
DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   019691;
01-NOV-1997 (Rel. 35, Created)
N-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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WormPep; F21H11.3; CE01245.
InterPro; IPR008967; P53-like.
InterPro; IPR001699; TF_T-box.
Pffm; PR00907; T-box.
PRINTS; PR00937; TBOX.
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HSSP; P24781; IXBR.
                                                                                                                                                                                                                                              60.0%;
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Matches 6; Conservative
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176 LVGLGGERAG 185
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Best Local Similarity
Matches 7; Conserva
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-|-
Xbb-, in which Xaa is preferably Leu, but may be other amino acids
including Pro although not Arg or Lys, and Xbb may be Pro.
-!- COFACTOR: Binds 2 manganese ions per subunit (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SUBLEARITY: Belongs to peptidase family M17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Woolwine S.C., Wozniak D.J.;
"Identification of an Escherichia coli pepA homolog and its
involvement in suppression of the algB phenotype in mucoid Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20437337; PubMed=10984043;
MEDLINE=20437337; PubMed=10984043;
MEDLINE=20437337; PubMed=10984043;
MEDLINE=20437337; PubMed=10984043;
Michel R. L., Michel R. S. L., Hufnagle W. O., Kowallk D. J., Lagrou M., Garber R. L., Goltry L., Tolentino E., Weetbrock-Wadman S., Yuan Y., Brody L. L., Coulter S. N., Folger K. R., Kas A., Larbig K., Lim R. M., Smith K. A., Spencer D. H., Wong G. K. -S., Wu Z., Paulsen I. T., Reizer J., Saier M. H., Hancock R. E. W., Lory S., Olson M. V.; "Complete genome sequence of Pseudomonas aeruginosa PAOI, an opportunistic pathogen.";
                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- FUNCTION: Presumably involved in the processing and regular turnover of intracellular proteins. Catalyzes the removal of unsubstituted N-terminal amino acids from various peptides (By
                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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66
MANGANESE 2 (BY SIMILARITY).
71
MANGANESE 1 AND 2 (BY SIMILARITY).
89
MANGANESE 2 (BY SIMILARITY).
48
MANGANESE 1 (BY SIMILARITY).
50
MANGANESE 1 AND 2 (BY SIMILARITY).
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InterPro; IPR000819; Peptidase_M17_C.
InterPro; IPR008293; Peptidase_M17_N.
Pfam; PF00893; Peptidase_M17, I.
Pfam; PF00491; Peptidase_M17, II.
PRINTS; PR00481; IAMNOPPTDASE.
PROSITE; PS00631; CYTOSOL_AP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99084946; PubMed=9864319;
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J. Bacteriol. 181:107-116(1999)
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EMBL, AE004800, AAG07218.1; -.
PIR, D83167, D83167.
                                                                                                                                                                                                                                                                                                                                                    Pseudomonadaceae; Pseudomonas
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                                                                                                                                                                                                   (Leucyl aminopeptidase).
PEPA OR PHPA OR PA3831.
                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa.
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SEQUENCE FROM N.A.
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Yersinia pestis.
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TRMU YERPE
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Shukla D.D., McKern N.M., Ward C.W.;

Shukla D.D., McKern N.M., Ward C.W.;

"Coat protein of potyviruses. 5. Symptomatology, serology, and coat protein sequences of three strains of passionfruit woodiness virus.";

Arch. virol. 102:221-222(1988).

-1- PIM: The viral RNA of potyviruses is expressed as a single polyprotein which undergoes posttranslational proteolytic processing resulting in the production of at least eight individual proteins.

-1- SIMILARITY: Belongs to the potyviruses polyprotein family.

RIR: C60078; VCVSWM.

RIR: PRO0767; Poty_coat.

R Pfam: PF00767; Poty_coat.

W Coat protein; Polyprotein.
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MEDLINE=22598143; PubMed=12712204;
Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia, J., Tu Y.-F.,
Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
                                                                                                                                                                                             Gaps
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Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Genome polyprotein [Contains Coat protein (CP)] (Fragment).
Passionfruit woodiness virus (strain Mild) (PWV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
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                                                                                                                               Length 495;
                                                                                                                                                                                          2; Indels
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278 POTENTIAL.
352 POTENTIAL.
52331 MW; E08C7928E7A0FCDC CRC64;
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                                                                                                                            Score 38; DB 1;
Pred. No. 64;
0; Mismatches
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10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
PEPLIGE Chain release factor 1 (RF-1).
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                                                                                                                        67.98;
                                                                                                                                                  80.08;
                                                                                                                                                      Local Similarity 80.0
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                                                                                                                                                                                                                                                                                                            433 IANIGGPKAG 442
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                             352 3
495 AA;
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Best Local Similarity
7; Conserv
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Q8F9S6;
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ACT_SITE
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RF1_LEPPN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no modifised and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A., Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z., Xu J.-G., Zhao G.-P., "Unique physiological and pathogenic features of Leptospira interrogans revealed by whole-genome sequencing."; Nature 422:88-893(2003).

-!- FUNCTION: Peptide chain release factor 1 directs the termination of translation in response to the peptide chain termination codons UNG and UAA (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
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MEDLINE=21470413; PubMed=11586360;

MEDLINE=21470413; PubMed=11586360;

MEDLINE=21470413; PubMed=11586360;

Parkhill J., Waren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable FRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
(EC 2.1.1.61).
TRMU OR YPO1638 OR Y1799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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TIGREAMS, TIGR00019; prfA, 1.
PROSITE; PS00745; RF PROK I; 1.
Protein biosynthesis; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.1%; Score 37; DB 1; 77.8%; Pred. No. 68; 1; Mismatches
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InterPro; IPR005139; PCRF.
InterPro; IPR00352; Pep_rel_factor_I.
InterPro; IPR004373; PrfA.
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STRAIN=KIMS / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF03462; PCRF; 1.
Pfam; PF00472; RF-1; 1.
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Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R., Perry R.D.;
                                                                                                   Perry R.D.;
"Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
-!- CATALYMIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-homocysteine + tRNA containing 5-methylaminomethyl-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ414149; CAC90460.1; -.
EMBL; AB013782; AAM85367.1; -.
PIK, A10199; A10199.
InterPro; IPR004506; TrmU.
Pfam; PF03054; tRNA Me_trans; 1.
TIGR0420; TIGR00420; TrmU, 1.
Transferase; Methyltransferase; tRNA processing; Complete proteome. SEQUENCE 371 AA; 41365 MW; D7A301D70B284F5F CRC64;
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66.1%; Score 37; DB 1; Length 371;
Best Local Similarity 77.8%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches 2; Indels
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Search completed: September 18, 2004, 04:26:24 Job time : 10.1961 secs

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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
51milar to collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Wakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
WCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 56; DB 4; Length 1163; ilarity 100.0%; Pred. No. 1.4; Conservative 0; Mismatches 0; Indels (
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Q7TPJ5
Q7XPP9
Q364PFT1
Q8PFT1
Q8PFT1
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Q9H5B2
Q7XXK9
Q9LC37
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Matches 11; Conservat
QBN6U4;
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Q9d3c5 mus musculu
Q9fri4 oryza sativ
Q7xcm3 oryza sativ
Q930j8 rhizobium m
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                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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seq length: 200000000
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Score

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STRAIN=CS7BL/6J; TISSUE=Head;
MBDLINE=22354683; PubMed=124668B1;
The FANTOM Consortium.

the RANTOM Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,700 full-length cDNAs.";
Nature 420:563-573 (2002).

EMBL; AK048546; BAC33370.1; -.

MGD; MG1:88453; Collagen; IEA.

GO; GO:0005581; C:collagen; IEA.

GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                          92.9%; Score 52; DB 11; Length 1222; 81.8%; Pred. No. 6.6; 1. Indels 0; Indels 0
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                                                                                                                                                                                                          1222 AA; 115140 MW; A409CA00D82765E4 CRC64;
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Last annotation update)
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Pred. No. 8;
2; Mismatches
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InterPro; IPR000885; Fib_collagen_C.
Pfam; PF01410; COLFI; 1.
Pfam; PF01391; Collagen; 16.
ProDom; PD002007; Clg helix; 1.
ProDom; PD002078; Fib_collagen_C; 1.
SWART; SW00038; COLFI; 1.
Hypothetical protein; Collagen.
NON TER 1
SEQUENCE 1222 AA; 115140 MW; A409G
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InterPro; IPR008160; Collagen.
InterPro; IPR00160; Collagen.
InterPro; IPR001805; Fib collagen_C.
InterPro; IPR001007; VWF_C.
Pfan; PF01391; Collagen; 18.
ProDom; PD000007; Clg helix; 1.
ProDom; PD0002078; Fib_collagen_C; 1.
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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les 9; Conservative
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MEDLINE=22254681; PubMed=12466851;
The FANTOM Consortium.
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Hemmer Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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MGD; MG1:88453; Collaga.1
GO; GO:005581; C:collagen; IEA.
GO; GO:005201; F:extracellular matrix structural constituent; IEA.
InterPro; IPR008160; Collagen.
InterPro; IPR008181; Fibrinogen.C.
InterPro; IPR00885; Fib. collagen.C.
Pfam; PF01410; COLFI; 1.
Pfam; PF01409; COLFI; 1.
Pfam; PF0140; COLFI; 1.
SMART; SM00038; COLFI; 1.
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GO, GO:0005581; C:collagen, IEA.
GO, GO:0005501; F:extracellular matrix structural constituent, IEA.
InterPro; IPR008161; Clq helix.
InterPro; IPR008160; Collagen.
InterPro; IPR002181; Fibrinogen_C.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Mammalia, Butheria, Rodentia, Sclurognathi, Muridae, Musinae, Mus
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                          Created)
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Best Local Similarity 81.0
                                          902 IAGIGGEKAGG 912
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
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                                                                                                                                                                                                                                                A STAIN-CSTBL/GAT TISSUE-Aorta, and Vein;

XX MEDLINE-22354683; PubMed=12466851;

A The FANTOM Consortium,

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A The FANTOM Consortium,

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A The FANTOM Consortium,

B MCD, MCI 184653; Collagen, IEA.

A MCD, MCI 184653; Collagen, IEA.

B MCD, MCI 184653; Collagen, C.

A InterPro; IPRO00161; Collagen.

B InterPro; IPRO00161; Fibrinogen.

C InterPro; IPRO00161; Fibrinogen.

B Ffam; PFO1410; Collagen; IB.

B PRODOM; PD000179; WF-C.

B Ffam; PFO1391; Collagen; IB.

B PRODOM; PD000179; Fibrolagen.C; I.

B RMART; SM00018; Col.Fij. I.

B SMART; SM00018; COLFI; I.

B B RMART; SM00018; COLFI; I.

B B RMART; SM00018; COLFI; I.

B B RMART; SM00149; WCC; I.
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STAIN-C2757BL/6; TISSUE-Brain;

A Klausner R.D., Peingold B.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

A Altschon M., Soaree M.B., Bonaldo M.F., Carainci P., Prange C.,

A Stapleton M., Soaree M.B., Bonaldo M.F., Carainci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Rah Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Rah Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1464 AA; 138939 MW; 91F3246D90818449 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Created)
Last sequence update)
Last annotation update)
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23,
25,
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1203 IAGVGGEKSGG 1213
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                        01-MAR-2003 (TrEMBLrel. 01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IAGIGGEKAGG 11
  01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein. Mus musculus (Mouse).
                                                                                                                      (Mouse)
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                       Collagen alpha 1.
                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Chayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDITRE-98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris I Gordon S.V., Eighmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Erown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Whole genome comparison of Mycobacterium tuberculosis clinical and
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.7%; Score 48; DB 11; Length 1464; ilarity 72.7%; Pred. No. 37; Conservative 2; Mismatches 1; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 1464 AA; 138971 MW; 2B38BC27AF21590B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC052398; AAH52398.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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FOLC OR RV2447C OR MTV008.03C OR MT2523.
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EMBL; AE007089; ARK46822.1; -.
EMBL; F70863; F70863.
HSSP; P15925; 1FGS.
TIGR; MT2523; -.
TUBECULIST; RASA47C; -.
TUBECULIST; RASA47C; -.
GO: GO: 0005524; F:AFF binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=C57BL/6; TISSUE=Brain;
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Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
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SEQUENCE FROM N.A.
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SEOUENCE 209 AA
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Q8L418;
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Matches
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               RRARRAR RRARRAR RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RRAPA RR
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GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0004326; F:tetrahydrofolylpolyglutamate synthase activity; IEA.
GO; GO:0009326; F:tetrahydrofolylpolyglutamate synthase activity; IEA.
GO; GO:0009396; P:folic acid and derivative biosynthesis; IEA.
InterPro; IPR001645; Fpolygl_synthse.
InterPro; IPR001045; Fpolygl_synthse.
InterPro; IPR001041; Mur_ligase.
Ffam, PF01225; Mur_ligase_C;
Ffam, PF01225; Mur_ligase_C;
Ffam, PF02875; Mur_ligase_C;
Ffam, PF02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
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Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, FR02875; Mur_ligase_C;
Ffam, Fr02875; Mur_ligase_C;
Ffam, Fr02875; Mur_ligase_C;
Ffam, Fr02875; Mur_ligase_C;
Ffam, Fr02875; Mur_ligase_C;
Ffam, Fr02875; Mur_ligase_C;
Ffam, Ffam, Ffam, Ffam, Ffam, Ffam, Ffam, Ffam, Ffam, Ffam, Ffam, Ffam, Ffam, Ffam, Ffam, Ffam, Ffam, Ffam, Ffam, Ffam, Ffam, 
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Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A., 100:7877-7882(2003).
Ligase; Complete proteome.
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Probable folylpolyglutamate synthase protein FOLC
(Folylpoly-gamma-glutamate synthetase) (FPGS) (EC 6.3.2.17).
FOLC OR MB2474C.
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Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae, Rhizobium/Agrobacterium group; Agrobacterium.
NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.6%; Score 44; DB 16; Length 487; 90.0%; Pred. No. 53; 1; Indels ive 0; Mismatches 1; Indels
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Last annotation update)
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MEDLINE=22709107; PubMed=12788972;
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Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
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Nester E.W.,
"The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21608551; PubMed=11743194; Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Goodner B., Hinkle G., Gattung S., Miller N., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.,
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01-0CT-2003 (TYENBLEE]. 23, Last amoctation update)
P0551A11.6 protein (OJ116 CO7.6 protein).
P0551A11.6 OR OJ116 CO7.6.
Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica sultivar-group).
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Ehrhartoideae; Oryzaae; Oryzaa.
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Sasaki I., Matsumoto I., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
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PIR; C98302; C98302.

O; GO:0003824; F:catalytic activity; IEA.

InterPro; IPR001087; Lipase GDSL.

Pfam; PF00657; Lipase GDSL, 1.
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Best_Local Similarity 70.0
Matches 7, Conservative
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Best Local Similarity 45.5
Matches 5; Conservative
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114 VSGVGGSRSGG 124
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                                                                                                                                                                                                                                                                                               2 AGIGGEKAGG 11
                                                                                                                                                                                                                                                                                                                     28 AGLGGRSAGG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4530;
                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                            Q9FRJ4;
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MEDLINE=21085660; PubMed=11217851;
Mawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
                                                                                                                                                                                                                                                                                                                                                                  Tauch A.;

"The IncP beta plasmid pB4 encodes a tripartite antibiotic efflux system of the RND-MFP-OEP type conferring erythromycin and roxithromycin resistance in Pseudomonas sp. Bl3.";

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ431260; CAD24375.1; -..

GO; GO:0046821; C:extrachromosomal DNA; IEA.

GO; GO:0009291; P:unidirectional conjugation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                 Score 41; DB 10; Length 208;
Pred. No. 68;
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                                                                                                            2; Indels
clone:OJ1116 C07.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003934; BAB92814.1; -.
EMBL; AP004253; BAC00689.1; -.
Gramene; QBL418; -.
SEQUENCE 208 AA; 20670 MW; C4D641DBA4D55B80 CRC64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  460 AA; 47889 MW; B88772672063B91D CRC64;
                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                 Gamma-proteobacterium Hot 75m4.
Plasmid pB4.
                                                                                    Query Match 73.2%;
Best Local Similarity 54.5%;
Matches 6; Conservative
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
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01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
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Best Local Similarity 60..
Best Local 6; Conservative
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211 SGVGGQQAGG 220
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63 VGGVGGREAGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF03743; TrbI; 1.
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5830493J20RIK.
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TRBI.
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Q8RSI9
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Radota K., Matsuda H.A., Ashburner M., Baralov S., Gasavant T., Fadeta K., Matsuda H.A., Ashburner M., Batalov S., Gasavant T., Fleischmann W., Gasafeerland T., Gissi C., King B., Kochiwa H., Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuki R., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchioni L., Mashima J., Mazarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodiguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., M. Hayashizaki Y., Runctional annotation of a full-length mouse cDNA collection.",
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,

Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,

Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,

Quackenbush J., White O., Salzberg S.L., Fraser C.M.;

"Oryza sattua chromosome 10 BAC OSJNBD0064P21 genomic sequence.";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AC073166; AAG46112.1;
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Gramene; O9FRJ4; -

Hypothetical protein.

Approximants 156 AA; 15960 MW; 22DDB710603858FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 AA; 13746 MW; B125F747DA12CFF2 CRC64;
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Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
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EMBL, AKO18067; BAB31058.1; -.
MGD, MGI:1923370; 5830493J20Rik.
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01-MAR-2003 (TEMBLrel. 16, La
01-CCT-2003 (TEMBLrel. 25, La
Hypothetical protein.
05JNBB0064P21.10.
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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

RATANI-1021;

RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,

Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,

RA Barnett M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,

RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,

RA K.-C., Davis R.W., Federspiel N.A., Long S.R.;

RA K.-C., Davis R.W., Federspiel N.A., Long S.R.;

RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;

RA Yen K.-C., Davis R.W., Federspiel N.A., Long S.R.;

RA Yen K.-C., Davis R.W., Federspiel N.A., Long S.R.;

RA Yen K.-C., Davis R.W., Federspiel N.A., Long S.R.;

RA Yen K.-C., Davis R.W., Federspiel N.A., Long S.R.;

Broch N. Sinorhizoblum meliloti pSymA megaplasmid.",

RBBL, AE007121; AAK64855.1; -.

BRBL, AE007121; AAK64855.1; -.

BR MSL, BESSEG, ESSSEG.

GO: GO:0046821; C:extrachromosomal DNA; IEA.

KW Hypothetical protein; Plasmid; Complete proteome.

SEQUENCE 298 AA; 28617 MW; 27C9E96FDDID2068 CRC64;

SEQUENCE 298 AA; 28617 MW; 27C9E96FDDID2068 LOGG S.
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                                                                                                     Oryza sativa (japonica cultivar-group).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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The Rice Chromosome 10 Sequencing Consortium;
"In-depth view of structure, activity, and evolution of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Sinorhizobium/Ensifer group, Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 10; Length 156;
Pred. No. 74;
5; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-cv. Nipponbare,
Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AE017116, AAP54848.1;
Hypothetical protein.
SEQUENCE 156 AA; 15960 MW; 22DDB710603858FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DTW-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein RA0197.
RA0197 OK SWA0367.
Rhizobium meliloti (Sinorhizobium meliloti)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
OSJNBB0064P21.10.
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Best Local Similarity 45.5%;
Matches 5; Conservative
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Science 300:1566-1569(2003)
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0930.8
ID 30.0
AC 0930.01
DT 01-DEW
DT 01-DEW
DT 01-DEW
DE HAPPOLL
GN RA019.0
OG Plasm
OC Rhizo.
OC Rhizo.
OC Rhizo.
CN NCEL
RA Barne
RA Barne
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RA Kalma
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Search completed: September 18, 2004, 04:29:41 Job time : 41.0392 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

(without alignments) 52.784 Million cell updates/sec September 18, 2004, 03:47:39; Search time 64.2353 Seconds Run on:

US-10-615-959-43 62 Title:

1 IAGIGGEKAGGF 12 **BLOSUM62** score: Scoring table: Sequence: Perfect

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

1586107 segs, 282547505 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genesequi980s:\* genesequi990s:\* genesequi2000s:\* genesequi2001s:\* genesequi2003s:\* genesequi2003bs:\* genesequi2003bs:\* A\_Geneseq\_29Jan04:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Aab61743 Human typ	Aae38632 Human C-t	Aae38640 Human col	Aay07375 Procollag	Abu70813 Human adi	Aau23675 Novel hum	Abg60248 Human ova	Novel		Aaw12843 Pro-alpha	Aaw12842 Truncated	Ade08475 Novel pro	Abb50291 Collagen	Abb90747 Human Tum	Abu54454 Human tum		Abg15191 Novel hum	Ade09399 Novel pro	Abr42661 Decorin-m	Aae02537 Porcine a	Aab61742 Human typ		Aay96125 Collagen	Aael6478 Human col	Abb80736 Collagen
SUMMARIES	ID	AAB61743	AAE38632	AAE38640	AAY07375	ABU70813	AAU23675	ABG60248	ABG61719	ABU70735	AAW12843	AAW12842	ADE08475	ABB50291	ABB90747	ABU54454	ABR47418	ABG15191	ADE09399	ABR42661	AAE02537	AAB61742	AAR71704	AAY96125	AAE16478	ABB80736
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	Score	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	61	95	26	26	26	26
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Abb09628 Amino aci Aae02534 Bovine al Aae02533 Bovine al Aar92068 Recombina	Aab61741 Human typ Aay68425 Type III Aay68436 Type III Aay82167 Type II a	1000		Abuiy644 Frocein e Aao00933 Human pol Aay34469 Porphorym	Aay34345 Porphorym Aaw71488 Helicobac Abu23506 Protein e
ABB09628 AAE02534 AAE02533 AAR92068	AAB61741 AAY68425 AAY68436 AAY82167	AAB51275 AAB61740 ABG08457			AAY34345 AAW71488 ABU23506
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### ALIGNMENTS

Human type III collagen carboxy-telopeptide fragment. AAB61743 standard; peptide; 12 AA (first entry) 20-APR-2001 AAB61743; RESULT 1 AAB61743

Type II collagen; immunoassay; cartilage; telopeptide; human; type III collagen.

WO200079284-A1. Homo sapiens. Synthetic.

99US-00335098. 99US-0141574P. 99US-0142274P. 99US-0142675P. 99US-00385740. 99WO-US029357. 10-DEC-1999; 02-JUL-1999; 07-JUL-1999; 30-AUG-1999; 17-JUN-1999; 29-JUN-1999; 28-DEC-2000. 

(WASH-) WASHINGTON RES FOUND.

Eyre DR;

WPI; 2001-146859/15.

Assay for detecting cross-linked telopeptide analytes indicative of type II collagen resorption in vivo in a body fluid sample, comprises contacting the sample with an antibody which binds to the analyte.

Disclosure; Page 15; 34pp; English.

The invention relates to immunoassays for measuring type II collagen (cartilage) resorption in vivo. The method of analysing a body fluid sample for the presence of an analyte indicative of a physiological condition, involves contacting the body fluid sample with an antibody (Ab) which binds to the analyte, detecting binding of Ab in the body fluid sample, and correlating any detected binding to the physiological condition. The analysis is useful for measuring type II collagen (cartilage) resorption in vivo, for distinguishing between resorption of

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The invention relates to a method of determining the rate of biosynthesis or breakdown of at least one inaccessible biological molecule in a subject. The method is useful for diagnosis or monitoring and treatment of diseases associated with an altered rate of biosynthesis/breakdown of an isotopically labelled precursor molecule, specifically osteoporosis; left-ventricular hypertrophy; liver cirrhosis or fibrosis; cardiac or lung fibrosis; Alzheimer's disease; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; muscle-wasting syndromes; mescular dystrophy; athletic gene or protein targets, phenotypic/human validation studies on potential drugs, drug mechanism studies and determining the risk of developing the disease. The present sequence is human C-terminal telopeptide alpha 1. This sequence is used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; therapy; osteoporosis; left-ventricular hypertrophy; scleroderma; liver cirrhosis; congestive heart failure; multiple sclerosis; fibrosis; coal-miner's pneumoconiosis; muscle-waeting syndrome; diabetes mellitus; rheumatoid arthritis; Alzheimer's disease; muscular dystrophy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determining rate of biosynthesis or breakdown of inaccessible biological molecules, useful e.g. for diagnosis or monitoring treatment, by administering labeled precursor.
non-mineralized and mineralized cartilage, and for measuring total cartilage resorption in vivo. The present sequence represents a linear synthetic peptide based on the carboxy-terminal telopeptide sequence of human collagen type III
                                                                                                                                                                 Gaps
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                                                                                                                          100.0%; Score 62; DB 4; Length 12; 100.0%; Pred. No. 0.0028; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                           AAE38632 standard; peptide; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-FEB-2003; 2003WO-US004183.
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Best Local Similarity
Local 12; Conservative
Local 12; Conservative
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                                                                                        Sequence 12 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Determining rate of biosynthesis or breakdown of inaccessible biological molecules, useful e.g. for diagnosis or monitoring treatment, by administering labeled precursor.
                                                                                                                                                                                                                                                                                        Human, therapy, osteoporosis, left-ventricular hypertrophy, scleroderma, liver cirrhosis, congestive heart failure; multiple sclerosis, fibrosis, coad-miner's pneumoconiosis, muscle-wasting syndrome, diabetes mellitus, rheumatoid arthritis, Alzheimer's disease; muscular dystrophy, cancer; collagen type I cross-linked carboxy-terminal peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease. The present sequence is human collagen type I cross-linked carboxy terminal peptide (ICTP). This sequence is used to illustrate the
                                                                                                                                                                                                                                                       Human collagen type I cross-linked C-terminal peptide, PIIICP(alphal).
Gaps
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Pred. No. 0.065;
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                                                                                                                                                    AAE38640 standard; protein; 262 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
12;
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Matches
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RESULT 4

Score 62; DB 7; Length 25; Pred. No. 0.006;

100.0%; 100.0%;

Query Match Best Local Similarity

Sequence 25 AA;

us-10-615-959-43.rag

(first entry)

10-JUN-2003

ABU70813;

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Page

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Diseases such as alcoholic cirrhosis, biliary cirrhosis, hepatitis, schistosomiasis, cardiac fibrosis, Crohn's disease, diabetic nephropathy and fibroses caused by surgery result from an inappropriate production of collagen fibrils. Collagen III is synthesised as a preproprotein which is modified by post-translation modification. The mature collagen III fibrils are generated by cleavage of a propeptide from the C-terminus followed by cleavage of a propeptide from the C-terminus corresponds to the procollagen III C-terminal propeptide (FIICP). As the fibrils are formed, the FIICP propeptide is released into the surrounding tissue fluids. The invention relates to an immunoassay to determine PIICP concentrations and thus diagnose the above diseases and others which result from inappropriate collagen deposition. Different fibrotic diseases may show different levels of FIICP in the serum so the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New immunoassay for procollagen-III-C-terminal propeptide (PIIICP) useful for diagnosing diseases such as alcoholic cirrhosis, hepatitis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunoassay may also be used to determine which disease a particular patient is suffering from. The new immunoassay may also be used to measure the rate of collagen synthesis in patients being treated with glucocorticosteroids. In addition the new antibodies may be used in immunohistochemical staining of cryostat and paraffin sections to assess collagen synthesis in tissue samples from patients suspected of having
                                                                                                                                                                              Alcoholic cirrhosis; biliary cirrhosis; hepatitis; schistosomiasis; cardiac fibrosis; Crohn's disease; diabetic nephropathy; collagen; fibril; procollagen-III-C-terminal propeptide; immunoassay; diagnosis; gluccorticosteroid; antibody.
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100.0%; Pred. No. 0.067;
tive 0; Mismatches 0; Indels
                                                                                                                                             Procollagen-III-C-terminal propeptide
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                        AAY07375 standard; protein; 270 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig 1, 28pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Duchenne's muscular dystrophy.
                                                                                                                                                                                                                                                                                                                                                                                                      97EP-00119018.
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                                                                                                     (first entry)
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nes 12; Conserv
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                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                     16-JUL-1999
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                                                              AAY07375;
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Matches
AAY07375
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Schroeder W;

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The invention relates to a complex between two interacting proteins in adipocyte cells, given in the specification. The proteins are identified by selecting a bait protein from a known adipocyte marker and then performing a yeast 2-hybrid selection to isolate prey proteins encoded by commence of an adipocyte cDNA library. The proteins are designated SID (RTM) (selected interacting domains) proteins. Also included are a polymetries of the complex, selecting a modulating compound in adipocyte colls, a recombinant host cell expressing at least one of the interacting colymeptides of the complex, selecting a modulating compound in adipocyte cells, a SID (RTM) polymeptide comprising any of the 738 amino acid sequences given in the specification (including its fragment or variant), cells, in the specification (including its fragment or variant), a vector comprising the SID (RTM) polymoleotide, a recombinant host cell comprising the Vector, a protein chip comprising the polypeptides and compounds are useful for the complex, polypeptides, polymeleotides and compounds are useful for man of the complex of the complex of the case of the complex of the case of the complex of the case of the complex of the case of the complex of the case of the complex of the case of the complex of the case of the complex of the case of the complex of the case of the complex of the case of the complex of the case of the complex of the case of the complex of the case of the complex of the case of the case of the case of the complex of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of the case of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New complex between two interacting proteins in adipocyte cells, useful for identifying selected interacting domains that modulate protein interactions, or for preventing or treating metabolic disorders such as obesity or diabetes.
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                                                                                                                                                        Human; prey; adipocyte; SID; selected interacting domain; anorectic;
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                                                                                                   Human adipocyte Selected Interacting domain, SID, #444.
                                                                                                                                                                                 antidiabetic, protein-protein interaction; diabetes; yeast 2-hybrid assay; metabolic disorder; obesity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Page 258-259; 382pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Daviet L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-103412/09.
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                                                                                                                                                                                                                                                                                                                    WO200286122-A2.
                                                                                                                                                                                                                                                                  Homo sapiens
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ABU70813 standard; protein; 293 AA.

ABU70813 ID ABU7 RESULT 5

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   Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; anti arthritic; nephrotropic; anticoagulant.
                                                                   Novel human enzyme polypeptide #761
                                                                                                                                                                                                                                                                                                                                                          31-JAN-2000; 2000US-0179065P.

24-FEB-2000; 2000US-0118652BP.

25-MAR-2000; 2000US-01186350P.

16-MAR-2000; 2000US-01186350P.

17-MAR-2000; 2000US-0118123P.

19-MAY-2000; 2000US-01390076P.

19-MAY-2000; 2000US-01391076P.

26-JUL-2000; 2000US-0215135P.

17-JUL-2000; 2000US-0215135P.

11-JUL-2000; 2000US-0215135P.

11-JUL-2000; 2000US-021647P.

07-JUL-2000; 2000US-021647P.

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11-JUL-2000; 2000US-021647P.

11-JUL-2000; 2000US-0215135P.

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11-JUL-2000; 2000US-021513FP.

11-JUL-2000; 2000US-021513FP.

14-JUC-2000; 2000US-0225264P.

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                                  (first entry
                                                                                                                                                                                                                                                              WO200155301-A2
                                                                                                                                                                                                                             Homo sapiens
                                18-DEC-2001
                                                                                                                                                                                                                                                                                             02-AUG-2001
AAU23675;
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The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or lygases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of diagnosis, treatment, prevention and/or prognosis of a wide range of disoncers (e.g. cancer), immunodeficiency disorders (e.g. cancer), immunodeficiency disorders (e.g. ALDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. AlDS) autoimmune disorders (e.g. arthritis), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. haemophila), reproductive disorders (e.g. infertility) and infectious disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polynucleotides of the invention can also be used in gene therapy, AMU22915-AMU23914 represent the novel human enzyme polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but he was betained an electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polypeptides and polynucleotides useful for diagnosing, preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; ovarian antigen, ovary disorder; breast disorder; neoplastic disorder; cancer; infectious disease; inflammatory disease; reproductive system disorder; autoimmune disorder; Alzheimer's disease; blood-related disorder; hyperproliferative disorder; hair loss; urinary system disorder; musculoskeletal system disorder; respiratory disorder; musculoskeletal system disorder; neural activity disorder; eucological disorder; endocrine disorder; gastrointestinal disorder; liver disorder; pancreatic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                            treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; SEQ ID NO 1671; 1180pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG60248 standard; protein; 309 AA.
                                                                                                                                                                                                                                                                                                              Barash SC, Ruben SM;
05-DEC-2000; 2000US-0251030P.

05-DEC-2000; 2000US-025198BP.

05-DEC-2000; 2000US-0251479P.

06-DEC-2000; 2000US-0251856P.

08-DEC-2000; 2000US-0251868P.

08-DEC-2000; 2000US-0251868P.

08-DEC-2000; 2000US-0251989P.

08-DEC-2000; 2000US-0251999P.

11-DEC-2000; 2000US-0251999P.

05-JAN-2001; 2001US-0251999P.
                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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N-PSDB; AAS41545.
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les 12; Conserv
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The invention relates to isolated ovarian related polypeptide (ovarian antigen) comprising a sequence at least 90% identical to a sequence selected from a polypeptide fragment, domain, epitope or full length protein of a sequence (51) appearing as ABG60239-ABG60266 having protein of a sequence (51) appearing as ABG60239-ABG60266 having condition in condition or species homologue of S1. Also included are the cDNA are useful for diagnosing, preventing, an anti-S1 antibody and the cDNA are useful for diagnosing, preventing, complastic disorders (such as ovarian Krukenberg tumour and cancer), infectious diseases (e.g., mastitis, oophoritis), inflammatory diseases (e.g., mastitis, oophoritis), inflammatory diseases (e.g., mastitis, oophoritis), inflammatory diseases (e.g., mastitis, oophoritis), inflammatory diseases (e.g., mastitis, oophoritis), inflammatory diseases (e.g., mastitis, oophoritis), inflammatory diseases (e.g., mastitis, oophoritis), inflammatory diseases (e.g., mastitis, oophoritis), inflammatory diseases (e.g., mastitis, oophoritis), inflammatory diseases (e.g., mastitis, oophoritis), inflammatory diseases (e.g., mastitis), cardiovascular disorders (sickle cell anaemia), respiratory disorders (Alatheimer's disease and Parkinson's disease), arthritis, cardiovascular disorders (sickle cell anaemia), respiratory disorders (Alatheimer's diseases and Parkinson's disease), endocrine disorders (Alatheimer's diseases and Parkinson's disease), candevolopmental and inherited disorders, disorders (bilary liver cirrhosis), coperce transplantation or for supporting cell cost, or mintain organs (before transplantation or for supporting cell cost, organized and subjust to change a mammal's mental or physical state, and covarian antigen, SI protein of the printed specification, but was conditive and indectronic format directly from WIPO at frequence data for this patent did not format directly from WIPO at frequence data for condition in electronic format directly from WIPO at frequence data for conditions and cond
gall bladder disorder, large intestine disorder; developmental disorder; inherited disorder; wound healing; skin aging; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated human ovarian related polypeptide useful for diagnosis/treatment of disorders of ovary and breast such as neoplastic disorders, infectious diseases, inflammatory diseases, and reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; SEQ ID NO 78; 524pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruben SM
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2000US-0251868P.
2000US-0251990P.
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2000US-0232398P.
2000US-0249300P.
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                                                                                                                                                                                                                                                                        2000US-0180628P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-476195/51.
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                                                                                                                         WO200155329-A2.
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14-SEP-2000;
17-NOV-2000;
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Sequence 309 AA;

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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                    Ovarian related polypeptide, neoplastic disorder; tumour; ovarian cancer; breast cancer; reproductive system disorder; tuberculosis; arthritis; immune system disorder; tuberculosis; arthritis; immune system disorder; the disorder; the disorder; the disorder; the disorder; system disorder; hashimoto's thyroiditis; inflammatory disorder; septic shock; multiple solerosis; central nervous system disorder; neurological disorder; allergy; Parkinson's disease; Alzheimer's disease; cardiovascular disorder; atherosclerosis; blood related disorder; respiratory disorder; atherosclerosis; blood related disorder; respiratory disorder; infarty system disorder; infectious disorder; osteoporosis; wound healing; endocrine disorder; infectious disease; gastrointestinal disorder; transplantation; food additive; preservative.
                                              Gaps
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    100.0%; Score 62; DB 4; Length 309; 100.0%; Pred. No. 0.077; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                       Novel ovarian related polypeptide #10
                                                                                                                                                                                                                   ABG61719 standard; protein; 309 AA.
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24-FEB-2000; 2000US-0184664P.
02-MAR-2000; 2000US-0184664P.
02-MAR-2000; 2000US-0188350P.
16-MAR-2000; 2000US-0189834P.
17-MAR-2000; 2000US-0198123P.
19-MAY-2000; 2000US-0198123P.
07-JUN-2000; 2000US-0198123P.
07-JUN-2000; 2000US-0214886P.
07-JUL-2000; 2000US-021488P.
11-JUL-2000; 2000US-021664P.
11-JUL-2000; 2000US-0218990P.
11-JUL-2000; 2000US-0218990P.
14-MUG-2000; 2000US-021819P.
14-AUG-2000; 2000US-0224518P.
14-AUG-2000; 2000US-0224518P.
14-AUG-2000; 2000US-0225266P.
14-AUG-2000; 2000US-0225266P.
14-AUG-2000; 2000US-0225266P.
14-AUG-2000; 2000US-0225266P.
14-AUG-2000; 2000US-0225266P.
14-AUG-2000; 2000US-0225266P.
14-AUG-2000; 2000US-0225266P.
14-AUG-2000; 2000US-0225266P.
14-AUG-2000; 2000US-0225268P.
14-AUG-2000; 2000US-0225268P.
14-AUG-2000; 2000US-02252758P.
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2000US-0226279P.
2000US-0226681P.
2000US-0226868P.
2000US-0227182P.
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                                                                                                                                                                                                                                                                                                 26-AUG-2002 (first entry)
Query Match
Best Local Similarity 100.
Matches 12; Conservative
                                                                                   1 IAGIGGEKAGGF 12
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22-AUG-2000;
22-AUG-2000;
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100.0%; Score 62; DB 5; Length 309; 100.0%; Pred. No. 0.077; ive 0; Mismatches 0; Indels
17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249216P.
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2001US-00764856.
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2000US-0249265P.
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2000US-0251856P.
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RUBIN S M.
BARASH S C.
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06-DEC-2000;
06-DEC-2000;
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11-DEC-2000;
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01-DEC-2000;
05-DEC-2000;
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(RUBI/)
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Matches
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The invention relates to a complex between two interacting proteins in adipocyte cells, given in the specification. The proteins are identified by selecting a bait protein from a known adipocyte marker and then performing a yeast 2-hybrid selection to isolate prey proteins encoded by members of an adipocyte colnA library. The proteins are designated SID (RTW) (selected interacting domains) proteins. Also included are a polymucleotide encoding a polypeptide in the adipocyte cells, a recombinant host cell expressing at least one of the interacting colypeptides of the complex, selecting a modulating compound in adipocyte cells, a SID (RTW) polypeptide comprising any of the 738 amino acid cells, a SID (RTW) polypucleotide comprising ny of the 738 mucleotide sequences given in the specification (including its fragment or variant), a SID (RTM) polypucleotide comprising the vector, a protein including its fragment or variant), a vector comprising the vector, a protein chip comprising the polypeptides and compounds are useful for preventing or treating metabolic disorders such as obesity or diabetes. The polymucleotides are useful as probes or primers. The complex is comprising the therapeutic effect. The present sequence represents a SID (RTW) protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New complex between two interacting proteins in adipocyte cells, useful for identifying selected interacting domains that modulate protein interactions, or for preventing or treating metabolic disorders such as obesity or diabetes.
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                                                                                                                                            Human; prey; adipocyte; SID; selected interacting domain; anorectic; antidiabetic; protein-protein interaction; diabetes; yeast 2-hybrid assay; metabolic disorder; obesity.
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                                                                                                           Human adipocyte Selected Interacting domain, SID, #366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
ABU70735 standard; protein; 339 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Page 229; 382pp; English.
                                                                                                                                                                                                                                                                                                                                                                         14-MAR-2001; 2001US-0275734P
                                                                                                                                                                                                                                                                                                                                        14-MAR-2002; 2002WO-EP003768
                                                                        (first entry)
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Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                (HYBR-) HYBRIGENICS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 339 AA;
                                                                                                                                                                                                                                                                WO200286122-A2.
                                                                                                                                                                                                                            Homo sapiens
                                                                        10-JUN-2003
                                                                                                                                                                                                                                                                                                   31-OCT-2002
                                     ABU70735;
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Novel pro:collagen mol. - comprising pro:collagen C-pro:peptide attached to an alien collagen alpha-chain or non-collagen material, useful e.g. for wound healing.
                                                                                    C-propeptide, recognition sequence; procollagen; monomer chain; therapy, trimerised pro-alpha chain; fibril; procollagen suicide; wound healing; fibrotic disease; human; chimeric protein.
                                                                   Pro-alphal(III):(I) CP chimeric protein.
                                                                                                                                                                                                                                                                                                            Example 1; Page 32-35; 69pp; English.
                 AAW12843 standard; peptide; 623 AA.
                                                                                                                                                                                                                        (UYMA-) UNIV VICTORIA MANCHESTER.
                                                                                                                                                                                       95GB-00017773.
96GB-00006152.
96GB-00012476.
                                                                                                                                                                       96WO-GB002122
                                                  (first entry)
                                                                                                                                                                                                                                          Kadler K;
                                                                                                                                                                                                                                                         WPI; 1997-179268/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 623 AA;
                                                  15-DEC-1997
                                                                                                                                     WO9708311-A1
                                                                                                                                                                       30-AUG-1996;
                                                                                                                     Homo sapiens
                                                                                                                                                                                                         14-JUN-1996;
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                                                                                                                                                                                                                                         Bulleid N,
                                 AAW12843;
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This sequence represents a chimeric procollagen molecule of the invention. This sequence has the procollagen C-prepropeptide from the pro-alphal(III) chain sequence. The C-alpha2(I) chain attended to the pro-alpha1(III) chain sequence. The C-propeptide is implicated in the assembly of the monomer chains into trimerised pro-alpha chains prior to cleavage of the N- and C-propeptides and formation of Collagen in fibril-forming pro-alpha chains. The C-propeptides determine the type-specific assembly of the moieties to which they are attached. The molecule of the invention comprises a first moiety, which is an alien collagen alpha-chain or a non-collagen material. The novel collagen molecule can be used for treatment or diagnosis in humans can expecially for the treatment of procollagen suicide, as an cabesive or implant, to promote (chronic) wound healing or fibroric diseases with reduced scarring or for use in photography, brewing, containing substitutions in the recognition site, may have significantly containing substitutions in the recognition site, may have significantly contain selection properties
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                                          Gaps
                                          0
             100.0%; Score 62; DB 2; Length 623; 100.0%; Pred. No. 0.16; ive 0; Mismatches 0; Indels
Query Match
Best Local Similarity lov...
Local Similarity lov...
                                                                  1 IAGIGGEKAGGF 12
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IAGIGGEKAGGF 376

365

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RESULT 11 AAW12842 ID AAW12842 standard; protein; 626 AA.

29-JAN-2004 (first entry)

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This sequence represents a truncated procollagen pro-alphal(III) chain that can be used in the procollagen molecules of the invention. The C-propeptide is implicated in the assembly of the monomer chains into trimerised pro-alpha chains prior to cleavage of the N- and C-propeptides and formation of collagen in fibril-forming pro-alpha chains. The C-propeptides determine the type-specific assembly of the moietries to which they are attached. The molecule of the invention comprises a first moietry which is an allen collagen attached to a second moiety, which is an allen collagen abha-chain or a non-collagen material. The novel collagen molecule can be used for treatment or diagnosis in humans and seases with reduced scarring or for use in photography, brewing, codebuffs or textiles. The novel collagen so textiles are novel collagen molecules, especially when containing substitutions in the recognition site, may have significantly altered properties and characteristics, such as different binding the containing substitutions in the recognition as different binding the containing substitutions in the recognitions and different binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel pro:collagen mol. - comprising pro:collagen C-pro:peptide attached to an alien collagen alpha-chain or non-collagen material, useful e.g. for wound healing.
                                                                                                                C-propeptide; recognition sequence; procollagen; monomer chain; therapy; trimerised pro-alpha chain; fibril; procollagen suicide; wound healing; fibrotic disease; human.
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Pred. No. 0.16;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 28-31; 69pp; English.
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                                                                                  Truncated pro-alpha1(III) chain.
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96GB-00006152.
96GB-00012476.
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                                                  (first entry)
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Best Local Similarity 100.
Matches 12; Conservative
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23-MAR-1996;
                                                 15-DEC-1997
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                 AAW12842;
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ADE08475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma;
                                                                                                                                                                                                                                                                                                                                                                                                                                Wang J;
Wang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collagen type III alpha-1 ovarian tumour marker protein, SEQ ID NO:72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                               novel gene; novel protein; tissue marker; molecular weight marker; chromosome marker; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ovarian tumour marker gene; human; overexpression; upregulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
Novel protein (useful for identifying genetic disorders) #630.
                                                                                                                                                                                                                                                                                                                                                                                                                                Goodrich RW, Ren F, Zhang J, Zhao QA, ehrman T, Weng G, Zhou P, Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 62; DB 7; Length 842; 100.0%; Pred. No. 0.21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID NO 1541; 1177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT, Asundi V, Goodrich RW, Ren F,
Ghosh M, Xue AJ, Wehrman T, Weng G, Zh
Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB50291 standard; protein; 1466 AA.
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Conservative 0;
                                                                                                                                                                                                                                               11-DEC-2001; 2001US-0339453F.
14-MAR-2002; 2002US-0365091F.
14-MAR-2002; 2002US-036584F.
12-APR-2002; 2002US-0372381F.
12-APR-2002; 2002US-0372615F.
22-APR-2002; 2002US-0372615F.
                                                                                                                                                                                                10-DEC-2002; 2002WO-US039555
                                                                                                                                                                                                                                                                                                                                                             2002US-0376045P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-569235/53
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Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the invention.
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                                                                                                                           WO2003054152-A2
                                                                                                                                                                                                                                                                                                                                                             24-APR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ghosh M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ma Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
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The invention relates to methods for diagnosing and prognosing ovarian tumours in an individual via the detection and mesavement of the expression of ovarian tumour marker genes (ABA83183-ABA83182, ABA83182, ABA831812, ABA83181, ABA83181 and ABA83183). The methods of the invention are useful for detecting an ovarian tumour in a patient, for identifying an individual at increased risk for developing ovarian cancer, in prognostic tests for assessing the relative severity of ovarian cancer, in tests for monitoring a patient in remission from ovarian cancer and in tests for monitoring disease status in a patient being treated for ovarian cancer. The methods can additionally be used to identify a particular tumour as being an ovarian tumour (i.e., an epithelial ovarian tumour selected from excisous cystadenomar, borderline serous tumour, mucinous cystadenocarcinoma, borderline serous tumour, mucinous cystadenocarcinoma, clear cell adenocarcinoma, clear cell adenocarcinoma, clear of expression) and were found to be overexpressed in a broad variety of ovarian epithelial tumour cells relative to normal ovariant epithelial cells. The marker genes are information and in mucinous pathways, in the regulation of cell propolation and in mucinous pathways, in the regulation are membrane-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
adenofibroma, Brenner tumour; serial analysis of gene expression; SAGE; immune response pathway; cell proliferation regulation; protein folding; membrane localised; secreted; therapeutic target; cytostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting and identifying ovarian tumor, identifying increased risk for developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proliferation and in protein folding, and many of these are membrane-
localised or secreted. In addition to their use as diagnostic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prognostic markers, the ovarian tumour marker genes or their encoded proteins may be used as therapeutic targets for the treatment and prevention of ovarian cancer. Sequences ABB50257-ABB50299 represent proteins encoded by ovarian tumour marker genes of the invention
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                                                                                                                                                                                                                                                   03-APR-2001; 2001WO-US010947.
                                                                                                                                                                                                                                                                                             03-APR-2000; 2000US-0194336P
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Matches 12; Conserv
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                                                                                                                                                            WO200175177-A2
                                                                                                                   Homo sapiens
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90745, ABB90745, ABB90745, ABB90745, ABB90745, ABB90745, ABB90745, ABB90745, ABB90745, ABB90745, ABB90745, ABB90745, ABB90745, ABB90745, They are useful for inhibiting tumour growth, neoangiogeneis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthrits and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL92042-041 and ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                  Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic; normal endothelial marker; pan-endothelial marker; immunostimulant; antiangiogenic; tumour; neoangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis; psotiasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
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                                                                                                        Human Tumour Endothelial Marker polypeptide SEQ ID NO 226.
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11-AUG-2000; 2000US-0224360P.
11-APR-2001; 2001US-0282850P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Conservative
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N-PSDB; ABL92101.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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New purified human transmembrane protein, designated as tumor endothelial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
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pan-endothelial marker; polycystic kidney disease; psoriasis; diabetic retinopathy; rheumatoid arthritis; tumour anglogenesis; necangiogenesis; immune response; cytostatic; antidiabetic; ophthalmological; antirheumatic; antiarthritic; antipsoriatic.
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06-FEB-2002; 2002US-0354262P.
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us-10-615-959-43.rai

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GenCore version 5.1.6
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sw model OM protein - protein search, using Run on:

September 18, 2004, 04:20:54; Search time 19.7647 Seconds (without alignments) 31.344 Million cell updates/sec

US-10-615-959-43 62 Perfect score: Title:

1 IAGIGGEKAGGF 12

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

389414 seqs, 51625971 residues Searched:

389414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued\_Patents AA:\*
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

	Description	Sequence 43. Appl	m	ζ,	42	21,	21,	21,	Sequence 21, Appl	20,	4		m	40,	288	Sequence 23643, A	56	4	36.		12	51	12	12	2	729	22715,	32499,
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5 Sequence	5 Sequence	Sequence	Sequence				Sequence	Sequence		Sequence	Sequence		Sequence				
US-09-252-991A-27825	US-09-252-991A-18925	US-08-164-614A-9	US-08-456-489B-9	US-09-252-991A-30027	US-09-252-991A-19986	US-09-252-991A-21790	US-08-164-614A-8	US-08-456-489B-8	US-09-252-991A-20486	US-08-164-614A-7	US-08-456-489B-7	US-09-252-991A-27809	US-09-252-991A-28570	US-09-252-991A-16765	US-09-252-991A-27188	US-09-252-991A-26608	US-09-252-991A-22021
725 4	968 4	219 1	219 2	227 4	310 4	336 4	379 1	379 2	463 4	468 1	468 2	555 4	811 4	927 4	1084 4	1504 4	851 4
61.3	61.3	59.7	59.7	59.7	59.7	59.7	59.7	59.7	59.7	59.7	59.7	59.7	59.7	59.7	59.7	59.7	58.9
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28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

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FACURENT INPORMATION:

APPLICANT: Eyre, David R.

TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS;
FILE REPRENCE: WROS-1-1820

CURRENT PAPLICATION NUMBER: US/10/009,999A

CURRENT FILING DATE: 2003-01-22

PRIOR APPLICATION NUMBER: PCT/US99/29357

PRIOR PILING DATE: 1999-12-10

PRIOR PILING DATE: 1999-12-10

PRIOR PILING DATE: 1999-06-29

PRIOR PILING DATE: 1999-06-29

PRIOR PILING DATE: 1999-06-29

PRIOR PILING DATE: 1999-07-02

PRIOR PILING DATE: 1999-07-02

PRIOR PILING DATE: 1999-07-02

PRIOR PILING DATE: 1999-07-03

PRIOR APPLICATION NUMBER: US 60/142,675

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

PRIOR PILING DATE: 1999-07-07

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OTHER INFORMATION: synthetic peptide corresponding to carboxy-terminal
OTHER INFORMATION: telopeptide sequence of human type III collagen
US-10-009-9998-43
                                                                    ; Sequence 43, Application US/10009999A; Patent No. 6602980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
US-10-009-999A-43
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0; Query Match
100.0%; Score 62; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00088;
Matches 12; Conservative 0; Mismatches 0; Indels 1 IAGIGGEKAGGF 12 ò

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Gaps

1 IAGIGGEKAGGF 12

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Sequence 3, Application US/09029348
Patent No. 6171827
GENERAL INFORMATION:
APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER
TITLE OF INVENTION: NOVEL PROCOLLAGENS US-09-029-348-3

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US-08-963-825-21
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Sequence 42, Application US/1000999A

Sequence 42, Application US/1000999A

Sequence 42, Application US/1000999A

Sequence 42, Application US/10009

GENERAL INFORMATION:

APPLICANT: Byre, David R.

TITLE OF INVENTION: SINTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS

FILE REFERENCE: WROS-1-18220

CURRENT APPLICATION NUMBER: DC1/10/009,999A

CURRENT FILING DATE: 2003-01-22

PRIOR APPLICATION NUMBER: US 09/335,098

PRIOR FILING DATE: 1999-12-10

PRIOR FILING DATE: 1999-06-29

PRIOR FILING DATE: 1999-06-29

PRIOR FILING DATE: 1999-07-02

PRIOR APPLICATION NUMBER: US 60/142,274

PRIOR APPLICATION NUMBER: US 60/142,675

PRIOR APPLICATION NUMBER: US 60/142,675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09029348

Patent No. 6171827

GENERAL INFORMATION:

APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER;

TITLE OF INVERTION: NOVEL PROCOLLAGENS

FILE REFERENCE: d087857PUS LISTING

CURRENT APPLICATION NUMBER: US/09/029,348

CURRENT APPLICATION NUMBER: 1998-05-07

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn Ver. 2.0
FILE REFERENCE: d087857PUS LISTING CURRENT PEPLICATION NUMBER: US/09/029,348 CURRENT FILING DATE: 1998-05-07 NUMBER OF SEQ ID NOS: 20 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 3 LENGTH: 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 2
LENGTH: 626
TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
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US-10-009-999A-42
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GENERAL INFORMATION:
APPLICANT: Qvist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: A Method and Use of the Method to Diagnose the Presence of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                         CTHER INFORMATION: synthetic peptide corresponding to carboxy-terminal; OTHER INFORMATION: telopeptide sequence of human type III collagen US-10-009-999A-42
                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                      90.3%; Score 56; DB 4; Length 11; 100.0%; Pred. No. 0.007; ive 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/963,825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
PRIOR APPLICATION NUMBER: US 09/385,740 PRIOR FILING DATE: 1999-08-30 NUMBER OF SEQ ID NOS: 45 SOFTWARE: Patentin version 3.2 SEQ ID NO 42 LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/187,319
FILING DATE: 21-OAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21, Application US/08963825 Patent No. 6110689
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IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21:
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INFORMATION FOR SEQ ID NO: 21
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                    1 IAGIGGEKAGG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IAGIGGEKAĞG 11
                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
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TYPE: amino acid
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Best Local Similarity
Patent No. 6342361
GENERAL INFORMATION:
APPLICANT: Qvist,
APPLICANT: Bonde,
                                                                                                                                                                                                             CITY: New York
STATE: New York
                                                                                                                                                                                                                                                     USA
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US-09-548-608-21
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Sequence 21, Application US/09500811

Sequence 21, Application US/09500811

Service 21, Application US/09500811

GENERAL INFORMATION:
APPLICANT: Qviet, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of CORRESPONDENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Darby & Darby PC
STREET: 805 THIRd Avenue
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Pred. No. 0.65;
0; Mismatches 1; Indels
                    DB 3; Length 1078;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,811
                 Score 56; DB 3;
Pred. No. 0.65;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY TORNATION:
NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21:
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                  90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
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                                                                                                                          1058 IAGIGAEKAGGF 1069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 236687
INFORMATION FOR SEQ ID NO:
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                                                    11; Conservative
                                                                                        1 IAGIGGEKAGGF 12
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TOPOLOGY: linear
MOLECULE TYPE: prote
ORIGINAL SOURCE:
                 Query Match
Best Local Similarity
Matches 11; Conserval
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: USA
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Best Local Simil
Matches 11; C
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US-09-570-573-21
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STATE: No
COUNTRY:
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; Sequence 21, Application US/09570573

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A Method for Assaying Collagen Fragments in Body Fluids, A Test Kit and Means for Carrying Out the Method and Use of the Method to Diagnose the Presence of Disorders Associated with the Metabolism of
              A Method for Assaying Collagen Fragments in Body Fluids, A Test Kit and Means for Carrying Out the Method and Use of the Method to Diagnose the Presence of Disorders Associated with the Metabolism of
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                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/570,573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: GOGOTIS, Adda C
REGISTRATION UNBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELEPHONE: 212-527-7700
TELEPHONE: 212-527-7700
TELEEX: 236687
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/09548608
Fatent No. 6355442
GENERALINFORMATION:
APPLICANT: Qvist, Per
TITLE OF INVENTION: A Method for As
TITLE OF INVENTION: Method and Use
TITLE OF INVENTION: Method and Use
TITLE OF INVENTION: Disorders Associated the Correspondences: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRGANISM: Homo sapiens
| IMMEDIATE SOURCE:
| CLONE: COLLAGEN ALPHA 1 (III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Darby & Darby PC STREET: 805 Third Avenue
                                                                                                                                                              ADDRESSEE: Darby & Darby PC STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                              ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1058 IAGIGAEKAGGF 1069
Martin
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                 TITLE OF INVENTION: A METITLE OF INVENTION: in FITTLE OF INVENTION: Discrete OF INVENTION: Discrete OF SEQUENCES: 21 CORRESPONDENCE ADDRESS:
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MOLECULE TYPE: protein
ORIGINAL SOURCE:
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NAME/KEY: MISC FEATURE OTHER INFORMATION: synthetic peptide corresponding to carboxy-terminal OTHER INFORMATION: telopeptide sequence of human type III collagen
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5473052-20
5473052-20
75 PATORIN NO. 5473052
75 APPLICANT: EYRE, DAVID R.
77 TITLE OF INVENTION: ANTIGEN-BINDING FRACMENTS OF AN ANTIBODY
75 TYPE-I COLLAGEN AMINO-TERMINAL TELOPEPTIDE
75 NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                              87.1%; Score 54; DB 4; Length 15; 100.0%; Pred. No. 0.019; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 41, Application US/10009999A Patent No. 6602980 GENERAL INFORMATION:
REFERENCE/DOCKET NUMBER: 94
TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 354-442
TELEPFAX: (415) 354-4752
                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 100.
                                                                                                                         LENGTH: 15 amino acids
                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 77.4 Best Local Similarity 100. Matches 9; Conservative
                                                                                                                                                            single
                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                 3 GIGGEKAGGF 12
                                                                                                                                                                                                                                                                                                                                                1 GIGGEKAGGF 10
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 IGGEKAGGF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IGGEKAGGF 9
                                                                                                                                          TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-009-999A-41
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Fatent No. 653450
GENERAL INFORMATION:
APPLICANT: Berg, Richard A
APPLICANT: Toman, David P
APPLICANT: Wallace, Donald
TITLE OF INVENTION: MUTATED RECOMBINANT COLLAGENS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: COLLAGEN CORPORATION
STRET: 2500 Faber Place
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/548,608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/278,774
FILING DATE: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 56; DB 4
Pred. No. 0.65;
0; Mismatches
                                                                                                                                                                                                                                                                                                                 4305/08701
                                                                                                                                                                              FILING JALB:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08'
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEPHONE: 212-527-7700
                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COLLAGEN ALPHA 1 (III)
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ATTORNEY/AGENT INPORMATION:
NAME: REFLETATION NUMBER: 36,644
                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 212-753-6237
TELEX: 236897
INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: 1:----
TUBETT

TOPOLOGY: 1:---
TUBETT

TOPOLOGY: 1:---
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Best Local Similarity 91.7%;
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IAGIGGEKAGGF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                  COMPUTER READABLE FORM:
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
                  USA
                                                                                                                                                                           FILING DATE
                                10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94303
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US-08-278-774-20
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                  COUNTRY:
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Sequence 23643, Application US/09252991A

Sequence 23643, Application US/09252991A

Parent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196_136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28805
LENGTH: 21
                                                                                                                                                                                                                       OTHER INFORMATION: synthetic peptide corresponding to carboxy-terminal; OTHER INFORMATION: telopeptide sequence of human type III collagen US-10-009-999A-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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llarity 63.6%; Pred. No. 30;
Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                              67.7%; Score 42; DB 4; Length 8; 100.0%; Pred. No. 3e+05; ive 0; Mismatches 0; Indels
PRIOR FILING DATE: 1999-07-07
PRIOR PEDLICATION NUMBER: US 09/385,740
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
SEQ ID NO 40
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 28805, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 8, Conservative
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                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                            4 IGGEKAGG 11
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Best Local Similarity
Matches 7; Conserv
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US-09-252-991A-28805
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APPLICANT:
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APLICANTON:
APRICHEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION:
APRICHE REFERENCE:
107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER: OS 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 227
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US-10-009-999A-40
Squence 40, Application US/10009999A
Patent No. 660280
GENERAL INFORMATION:
TILLE NEPELCANT: BAYE, David R.
TILLE REFERENCE: WROS-1-18220
CURRENY APPLICATION NUMBER: US/10/009,999A
CURRENY APPLICATION NUMBER: US/10/009,999A
CURRENY APPLICATION NUMBER: US/10/009,999A
PRIOR FILING DATE: 1999-12-10
PRIOR FILING DATE: 1999-12-10
PRIOR PLILING DATE: 1999-06-29
PRIOR PLILING DATE: 1999-06-29
PRIOR PLILING DATE: 1999-06-29
PRIOR PLILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-07-02
PRIOR PLILING DATE: 1999-07-02
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                                                                                                                                                                                                                                                                                                                              Length 11;
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                                                                                                                                                                                                                                                                                                                              Score 48; DB 6;
Pred. No. 0.12;
0; Mismatches
                       APPLICATION NUMBER: US/08/221,705
FILING DATE: 01-ARP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 614,719
FILING DATE: 21-NOV-1990
APPLICATION NUMBER: 444,881
FILING DATE: 01-DEC-1989
APPLICATION NUMBER: 118,234
FILING DATE: 06-NOV-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Sequence 30541, Application US/09252991A ; Patent No. 6551795
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58.3%;
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158 LAGAGGDRRGGF 169
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Best Local Similarity 90.0
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Matches 7; Conservative
       CURRENT APPLICATION DATA:
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US-09-252-991A-30541
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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23643
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0; Gaps Query Match 66.1%; Score 41; DB 4; Length 503; Best Local Similarity 70.0%; Pred. No. 67; Matches 7; Conservative 2; Mismatches 1; Indels

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2 AGIGGEKAGG 11 ||:||:||| 481 AGLAGERAGG 490

QC δ

Search completed: September 18, 2004, 04:32:23 Job time: 19.7647 secs

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(without alignments)
67.677 Million cell updates/sec
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| cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/US06 NEW PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/US06 PUBCOMB.pep:*
| cgn2 6/ptodata/2/pubpaa/US06 PUBCOMB.pep:*
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| cgn2 6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US60_PUBGOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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62
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                                                                                                                                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 43, Appl	Sequence 11, Appl	Sequence 19, Appl	Sequence 78, Appl	Sequence 226, App	Sequence 72, Appl	Sequence 68, Appl	Sequence 33, Appl	Sequence 3, Appli	Sequence 3, Appli	10.	Sequence 12, Appl	Sequence 12, Appl	Sequence 42, Appl	Sequence 21, Appl
SUMMARIES	US-10-615-959-43	US-10-366-125-11	US-10-366-125-19	US-09-908-711-78	US-09-918-715-226	US-10-257-021-72	US-10-177-293-68	US-10-301-822-33	US-10-357-851-3	US-10-358-024-3	US-10-734-564-103	US-10-402-089-12	US-10-402-072A-12	US-10-615-959-42	US-10-058-124-21
	12	15	15	6	12	12	14	14	16	16	16	12	15	12	14
% Query Aatch Length DB	12	25	262	309	1466	1466	1466	1466	1466	1466	1466	1466	1466	11	1078
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Score	62	62	62	62	62	62	62	62	62	62	62	61	61	26	26
Result No.	-	7	e	4	ιΩ	9	7	∞	σ	10	11	12	13	14	15

16	55	88.7	1466	15	US-10-402-089-4	Sequence 4, Appli
17	55	88.7	1466	15	US-10-402-089-6	Sequence 6, Appli
18	55	88.7	1466	15	0-4	
19	52	88.7	1466	15	US-10-402-072A-6	Sequence 6, Appli
20	48	77.4	σ	12	US-10-615-959-41	
21	45	72.6	284	12	US-10-425-114-55247	Sequence 55247, A
22	43	69.4	225	16	US-10-437-963-106003	
23	42	67.7	80	12	- 1	Sequence 40, Appl
24	42	67.7	80	16	US-10-437-963-196331	_
25	42	67.7	112	16	US-10-437-963-139908	Sequence 139908,
26	42	67.7	847	12	US-10-425-114-55135	Sequence 55135, A
27	41	66.1	49	16	37	Sequence 163129,
28	41	66.1	105	16	US-10-767-701-37543	Sequence 37543, A
29	41	66.1	198	16	963-1	11439
30	41	66.1	228	12	US-10-627-476-402	Sequence 402, App
31	41	66.1	238	12	US-10-425-114-37899	
32	41	66.1	340	16	10-767-7	
33	41	66.1	691	12	US-10-282-122A-47568	Sequence 47568, A
34	40		105	16	10-767-701-3	10
35	40	64.5	107	12	US-10-425-114-37950	Sequence 37950, A
36	40	64.5	284	16	US-10-437-963-128057	Sequence 128057,
37	40	-	300	12	US-10-425-114-47773	
38	40		304	12	US-10-425-114-61720	
39	40	•	438	10	US-09-988-067B-30	Sequence 30, Appl
40	40		438	12	US-10-335-977-6127	Sequence 6127, Ap
41	40	•	441	12	US-10-335-977-6128	Sequence 6128, Ap
42	40	•	467	12	US-10-425-114-70808	708
43	40	64.5	471	12	US-10-425-114-64617	Sequence 64617, A
44	40	64.5	479	12	-10-282-122	$\sim$
45	40	64.5	969	16	US-10-437-963-189506	Sequence 189506,

### ALIGNMENTS

GENERAL INCOMEATION:

APPLICANT: Eyree, David R.

TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS
FILE REFERENCE: WROS-1-18220
CURRENT APPLICATION NUMBER: US/10/609,999A
PRIOR APPLICATION NUMBER: US/10/009,999A
PRIOR PLILING DATE: 2003-01-22
PRIOR PLILING DATE: 1999-12-10
PRIOR PLILING DATE: 1999-06-17
PRIOR PLILING DATE: 1999-06-17
PRIOR PLILING DATE: 1999-06-17
PRIOR PLILING DATE: 1999-06-17
PRIOR PLILING DATE: 1999-06-17
PRIOR PLILING DATE: 1999-06-29
PRIOR PLILING DATE: 1999-06-29
PRIOR PLILING DATE: 1999-06-29
PRIOR PLILING DATE: 1999-07-02
PRIOR PLILING DATE: 1999-07-02
PRIOR PLILING DATE: 1999-07-02
PRIOR PLILING DATE: 1999-07-02
PRIOR PLILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PATENTIN Version 3.2
SEQ ID NO 43 ; OTHER INFORMATION: synthetic peptide corresponding to carboxy-terminal; OTHER INFORMATION: telopeptide sequence of human type III collagen US-10-615-959-43 Sequence 43, Application US/10615959 Publication No. US20040048321A1 GENERAL INFORMATION: NAME/KEY: MISC\_FEATURE ORGANISM: Homo sapiens FEATURE:

100.0%; Score 62; DB 12; Length 12; 100.0%; Pred. No. 0.0054; Query Match Best Local Similarity

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NS-10-366-125-19

NS-10-366-125-19

Sequence 19, Application US/10366125

Publication No. US203228259A1

GENERAL INFORMATION:

APPLICANT: Hellerstein, Marc

ITILE OF INVENTION: MEASUREMENT OF BIOSYNTHESIS AND BREAKDOWN RATES OF

ITILE OF INVENTION: BIOLOGICAL MOLECULES THAT ARE INACCESSIBLE OR NOT

ITILE OF INVENTION: BY LABEL INCORPORATION INTO METABOLIC DERIVATIVES AND

ITILE OF INVENTION: CATABOLITIC PRODUCTS

ITILE OF INVENTION: CATABOLITIC PRODUCTS

FILE REFERENCE: 416272003500

CURRENT FILING DATE: 2003-02-12

PRIOR APPLICATION NUMBER: US 60/356,008
                                                                                                                                                                                               Sequence 11. Application US/10366125

Publication No. US20030226259A1

GENERAL INFORMATION:
TUTLE OF INVENTION: MEASUREMENT OF BIOSYNTHESIS AND BREAKDOWN RATES OF
TITLE OF INVENTION: BIOLOGICAL MOLECULES THAT ARE INACCESSIBLE OR NOT ITLE OF INVENTION: BASILY ACCESSIBLE TO DIRECT SAMPLING, NON-INVASIVELY,
TITLE OF INVENTION: CATABOLITY PRODUCTS
TITLE OF INVENTION: CATABOLITY PRODUCTS

FILE REFERENCE: 416272003500

CURRENT APPLICATION NUMBER: US/10/366,125

CURRENT FILING DATE: 2003-02-12

PRIOR FILING DATE: 2002-02-12

PRIOR FILING DATE: 2002-02-12

NUMBER OF SEQ ID NOS: 28

SOFTWARE: FASISE FASISE OF Windows Version 4.0

SEC ID NO. 11
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Mismatches
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 262
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                                                                           12; Conservative
                                         1 IAGIGGEKAGGF 12
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ORGANISM: Homo sapiens

US-10-366-125-11
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ORGANISM: Homo sapiens
US-10-366-125-19
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Best Local Similarity
Matches 12; Conserv
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Best Local Similarity
Matches 12; Conserv
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Sequence 68, Application US/10177293
Publication No. US20030124128A1
GENERAL INFORMATION:
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Hoersch, Sebastian
Monahan, John
Meyers, Rachel E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gannavarpu, Manjula
Kamatkar, Shubhangi
Mertens, Maureen
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Wang, Youzhen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lillie, James
APPLICANT: Glatt, Karen
APPLICANT: Zhao, Xumei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEO ID NO 72
LENGTH: 1466
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-257-021-72
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LOCATION: (2)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-908-711-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 62; DB 9; Length 309; 100.0%; Pred. No. 0.14; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 226, Application US/09918715

Publication No. US20030017157A1

GENERAL INFORMATION:

APPLICANT: Brad St. Croix

APPLICANT: Brad St. Croix

APPLICANT: Brad St. Croix

APPLICANT: Brad St. Croix

TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS

FILE REFERENCE: 1107.00134

CURRENT APPLICATION NUMBER: 00/09/918,715

CURRENT APPLICATION NUMBER: 60/22,599

PRIOR PILING DATE: 2000-08-02

PRIOR APPLICATION NUMBER: 60/224,360

PRIOR PELING DATE: 2000-08-11

PRIOR PELING DATE: 2000-08-11

PRIOR PELICATION NUMBER: 60/282,850

PRIOR PELICATION NUMBER: 60/282,850

PRIOR PELICATION NUMBER: 60/282,850

PRIOR PELICATION NUMBER: 60/282,850

PRIOR FILING DATE: 2000-08-11

PRIOR FILING DATE: 2000-04-11

NUMBER OF SEQ ID NOS: 358

SOFTWARE: FRAESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01312
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179, 065
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 167
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 78
LENGTH: 309
TYPE: PRT
CREATH: 309
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-226
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Matches 12; Conserva
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US-10-257-021-72
; Sequence 72, Application US/10257021
; Publication No. US20030211498A1
; GENERAL INFORMATION:

RESULT 6

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us-10-615-959-43.rapb

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Sequence 3, Application US/10358024

Publication No. US20040151732A1

GENERAL INFORMATION:

APPLICANT: Jicha, Douglas L.

APPLICANT: Pelsue, Stephen

TITLE OF INVENTION: Methods and Compositions Involving Blood

TITLE OF INVENTION: T-Lymphocytes Reactivity with Collagen

FILE REPERENCE: 1343640

CURRENT PILING DATE: 2003-02-04

CURRENT PILING DATE: 2003-02-04

NUMBER OF SEQ ID NOS: 3

SOFTWARE: FastSEQ for Windows Version 4.0
                                                  ; Score 62; DB 16; Length 1466;
; Pred. No. 0.67;
0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Score 62; DB 16; Length 1466;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 12; Conservative 0; Mismatches 0: Indale 0
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| Publication No. US20040157278A1
| GENERAL INFORMATION:
| APPLICANT: Christopher C Burgess et al.
| TITLE OF INVENTION: Detection Methods Using TIMP1
| FILE REFERENCE: 1657/2012
| CURRENT APPLICATION UNDER: US/10/734,564
| CURRENT APPLICATION UNDER: US/10/734,564
| CURRENT FILING DATE: 2003-12-12
| NUMBER OF SEQ ID NOS: 138
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 103
| LENGTH: 1466
                                                        Query Match
Best Local Similarity 100.0%;
Matches 12; Conservative 0
                                                                                                                                                                                                                1205 IAGIGGEKAGGF 1216
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Matches 12; Conservative
                                                                                                                                                                               1 IAGIGGEKAGGF 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-358-024-3
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US-10-358-024-3
        US-10-357-851-3
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GEQUENCE 33, Application US/10301822

Publication No. US2030148410A1

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: Berger, Allison

APPLICANT: Guillemette, Tracy L.

APPLICANT: Guillemette, Tracy L.

APPLICANT: Monahan, John E.

APPLICANT: Monahan, John E.

APPLICANT: Monahan, John E.

APPLICANT: Mibodeau, Stephen N.

APPLICANT: Mibodeau, Stephen N.

APPLICANT: Thibodeau, Stephen N.

APPLICANT: Thibodeau, Stephen N.

APPLICANT: Monahan, John E.

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND

TITLE OF INVENTION: NOVEL GENES, COMPOSITION, ASSESSMENT, PREVENTION, NOVELS, TITLE OF INVENTION: NOVELS: US 60/339, 971

FRIOR APPLICATION NUMBER: US 60/361, 978

PRIOR PLING DATE: 2002-01-21

PRIOR FILING DATE: 2002-01-22

PRIOR FILING DATE: 2002-01-22

PRIOR FILING DATE: 2002-03-05

PRIOR FILING DATE: 2002-05-20

NUMBER OF SEQ ID NOS: 228

NUMBER OF SEQ ID NOS: 228

SECTION 13
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Publication No. US2004015131A1

GENERAL INFORMATION:

APPLICANT: Jicha, Douglas L.

APPLICANT: Jicha, Douglas L.

TITLE OF INVENTION: Method and Compositions Involving

TITLE OF INVENTION: Abdominal Aortic Aneurysm Patients

TITLE OF INVENTION: Abdominal Aortic Aneurysm Patients

CURRENT APPLICATION NUMBER: US/10/357,851

CURRENT FILING DATE: 2003-02-04

NUMBER OF SEQ ID NOS: 3

SOFTWARE: FRAELSEQ for Windows Version 4.0
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                                                                                                                 Query Match 100.0%; Score 62; DB 14; Length 1466; Best Local Similarity 100.0%; Pred. No. 0.67; Matches 12; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 62; DB 14; Length 1466; Best Local Similarity 100.0%; Pred. No. 0.67; Matches 12; Conservative 0; Mismatches 0; Indels 0
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-68
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US-10-357-851-3
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100.0%; Score 62; DB 16; Length 1466; 100.0%; Pred. No. 0.67; 0; Mismatches 0; Indels 0
                                                                                                                                                                                RESULT 12
US-10-402-089-12
; Sequence 12, Application US/10402089
; Publication No. US20040005663A1
; GENERAL INFORMATION:
; APPLICANT: Bell, Marcum P.
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TYPE: PRT ORGANISM: Homo Sapiens

LENGTH: 1466

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FILING DATE: 1999-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-10-058-124-21
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                                                                                                                                                                                                                                         SEQ ID NO 42
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Publication No. US20040048321A1

GENERAL INFORMATION:

APPLICANT: Byre, David R.

TILLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS

TILLE REPERENCE: WROS-1-18220

CURRENT APPLICATION NUMBER: US/10/615,959

CURRENT FILING DATE: 2003-07-08

PRIOR FILING DATE: 2003-01-22

PRIOR APPLICATION NUMBER: PCT/US99/29357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 15; Length 1466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
APPLICANT: Neff, Thomas B.
APPLICANN: Polarek, James W.
APPLICANT: Seeley, Todd W.
TITLE OF INVENTION: PORCINE COLLAGENS AND GELATINS
FILE REFERENCE: FP0402.3 CON
CURRENT APPLICATION NUMBER: US/10/402,089
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US 09/709,700
PRIOR APPLICATION NUMBER: US 08/709,700
PRIOR APPLICATION NUMBER: US 08/709,700
SOFTWARE: PatentIn version 3.2
SOFTWARE: PatentIn version 3.2
SEQ ID NO 12
LEMETH: 1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sell, Marcum P.
APPLICANT: Bell, Marcum P.
APPLICANT: Neff, Thomas B.
APPLICANT: Neff, Thomas B.
APPLICANT: Selsey, Todd W.
TITLE OF INVENTION: BOVINE COLLAGENS AND GELATINS
FILE REFRENCE: FP0402.2 CON
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US 09/709,700
PRIOR PILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 61; DB 15
Pred. No. 0.94;
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PRIOR APPLICATION NUMBER: US 09/335,098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 12, Application US/10402072A
; Publication No. US20040018592A1
; GENERAL INFORMATION:
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91.7%;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Sus scrofa
                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-402-089-12
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US-10-615-959-42
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TITLE OF INVENTION: A Method for Assaying Collagen Fragments in Body Fluids, A Test Kit and Means for Carrying Out the Method and Use of the Method to Diagnose the Presence of Disorders Associated with the Metabolism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: synthetic peptide corresponding to carboxy-terminal OTHER INFORMATION: telopeptide sequence of human type III collagen
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WEBIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/058,124
FILING DATE: 29-Jan-2002
CIASSIFCATION: «Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/570,573
FILING DATE: 2002-MAY-12
APPLICATION NUMBER: 08/187,319
FILING DATE: «Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 90.3%; Score 56; DB 12; Length 11; Best Local Similarity 100.0%; Pred. No. 0.041; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INPORMATION:
NAME: GGOZIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
PRIOR APPLICATION NUMBER: US 60/141,574
PRIOR FILING DATE: 1999-06-29
PRIOR PLILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-07-02
PRIOR PLILING DATE: 1999-07-02
PRIOR PLILING DATE: 1999-07-07
PRIOR PELING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSES: Darby PC
STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21, Application US/10058124 Publication No. US20030119058A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Qvist, Per
Bonde, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IAGIGGEKAGG 11
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                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: MISC FEATURE
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0; Gaps
                                                                                                                                                                                                                                                                                                  Query Match 90.3%; Score 56; DB 14; Length 1078; Best Local Similarity 91.7%; Pred. No. 4; Matches 11; Conservative 0; Mismatches 1; Indels 0
| LENGTH: 1078 amino acids | TYPE: amino acids | TYPE: amino acid | TYPE: amino acid | TOPOLOGY: linear | TOPOLOGY: linear | ORGINAL SOURCE: | ORIGINAL SOURCE: | IMMEDIATE SOURCE: | CLONE: COLLAGEN ALPHA 1 (III) | SEQUENCE DESCRIPTION: SEQ ID NO: 21: US-10-058-124-21
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0;

Search completed: September 18, 2004, 04:56:14 Job time: 57.9412 secs

||||| ||||| 1058 IAGIGAEKAGGF 1069 1 IAGIGGEKAGGF 12

q ઠે

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

September 18, 2004, 04:02:05; Search time 14.5882 Seconds (without alignments) 79.125 Million cell updates/sec

US-10-615-959-43 62 Perfect score: Title:

Scoring table:

1 IAGIGGEKAGGF 12

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283366 segs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

LES	Description				r١	probable folylpoly	case		probable S2P metal	PBSX prophage ORF	calcium channel pr	formylmethanofuran	formylmethanofuran	hypothetical prote	conserved hypothet	hypothetical prote		c	hypothetical prote	hypothetical prote	homeobox protein -	conserved hypothet	hypothetical prote	probable exported	probable beta-gluc	hypothetical prote	calcium channel al	glycine-rich prote	halocyanin precurs	himothetical prote
SUMMAKIES	ΙD	HU7	S41067	859856	S14998	F70863	AE2981	C98302	G72777	F69732	A37860	H69074	S57457	E95286	C64654	H71943	T51035	T14302	T47394	T27543	149754	H95240	A99705	AF0169	T37843	H70599	T30535	T08002	F84274	G70691
	DB	п	7	7	7	7	7	7	7	7	7	~	7	~	7	7	~	7	7	~	7	N	7	~	7	7	~	7	~	7
	Length	1466	969	1464	161	487	209	209	383	1332	1852	270	270	298	438	438	548	87	163	175	399	605	605	622	636	846	1559	151	205	302
•	% Query Match	100.0		93.5	ij		67.7	٠.	66.1	66.1				64.5		64.5			62.9			62.9						ä	61.3	61.3
	Score	62	58	58	44	44	42	42	41	41	41	40	40	40	40	40	40	39	39	39	39	39	39	39	39	39	39	38	38	38
	Result No.	-	7	ო	4	S	9	7	Ф	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59

circumsporozoite p leukosialin precur	protein F21H11.3 [	leucine aminopepti	hypothetical glyci	RNA/ssDNA-binding	hypothetical prote	hypothetical prote	hypothetical prote	phage lambda-relat	hypothetical prote	coat protein - pas	hypothetical prote	hypothetical prote	hypothetical prote	probable ATP-bindi
OZZQAL	B88450	D83167	F70971	S71954	T00148	T30023	T29390	T14966	AI1951	VCVSWM	T33925	AB3091	H98195	E83622
н -	(7)	7	7	7	7	7	7	7	7	Н	N	N	7	0
378	423	495	588	589	694	875	935	1545	126	269	276	278	278	279
61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	61.3	59.7	59.7	59.7	59.7	59.7	59.7
38	8 6	38	38	38	38	38	38	38	37	37	37	37	37	37
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

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A904		
\$59511;		· · · · ·
RESULT 1 CGHU71  COGHU71  CABUTATA  CALABER alpha 1(III) chain precursor - human  N'Alternate names: procollagen alpha 1(III) chain  C.Species: Homo sapiens (man)  C.Species: Homo sapiens (man)  C.Species: Homo sapiens (man)  C.Species: A-Apr-1984 #sequence revision 01-Sep-1995 #text change 21-Jul-2000  C.Accession: S05272, S04642, PE0011, S01726, S04887; A90399, A94562, I51868; S59511; A904	R;Prockop, D.J. Bubmitted to the EMBL Data Library, February 1989 A;Reference number: S05272 A;Accession: S05272 A;Accession: preliminary A;McTeuts: preliminary	A;Residues: 1-1240, 'V',1242-1466 <prc> A;Cross-references: EMBL:X14420; NID:g30057; PIDN:CAA32583.1; PID:g30058 R;Ala-Kokko, L.; Kontusaari, S.; Baldwin, C.T.; Kuivaniemi, H.; Prockop, D.J. Biochem. J. 260, 509-516, 1989</prc>
RESULT 1 CGHU7L collagen aly N,Alternate C,Species: B C,Date: 24-7 C,Accession:	Ribrockop, D.J. submitted to the EMBL A;Reference number: SC A;Accession: S05272 A;Status: preliminary A:Molecule from: MRNA	A;Residues: 1 A;Cross-refer R;Ala-Kokko, Biochem. J. 2
K002000	្យស្សស្ស	; «; «; ¤; m) «

A; Title: Structure of cDNA clones coding for the entire prepro-alphal(III) chain of humar

A;Reference number: S04642; MUID:89350838; PMID:2764886 A;Accession: S04642

A;Molecule type: mRNA A;Residues: 1-1196 <ALA> A;Cross-references: EMBL:X14420; NID:g30057; PIDN:CAA32583.1; PID:g30058

A;Note: the complete sequence is not shown
R;Benson-Chanda, V.; Su, M.W.; Weil, D.; Chu, M.L.; Ramirez, F.
Gene 78, 252-265, 1989
A;1tle: Cloning and analysis of the 5' portion of the human type-III procollagen gene ((

A, Accession: PE0011

A; Molecule type: DNA
A; Residues: 1-176 < BEN>
A; Cross-references: GBNA
A; Cross-references: GBNA
A; Cross-references: GBNA
Cross-references: GBNA
Cross-references: GBNA
Cross-references: GBNA
Cross-references: GBNA
Cross-reference
Nucleic Acids Res. 16, 7201, 1988
A; Title: Nucleotide sequence of a cDNA coding for the amino-terminal region of human pref.
A; Reference number: S01726; MUID:88303360; PMID:3405773
A; Recession: S01726

A,Molecule type: mRNA A,Residues: 1-170 < TON. A,Residues: 1-170 < TON. A,Cross-references: EMBL:X07240; NID:930060; PIDN:CAA30229.1; PID:930061 A,Note: the authors translated the codon CAG for residue 154 as His R;Janeczko, R.A.; Ramirez, F. Nucleic Acids Res. 17, 6742, 1389 A;Title: Nucleotide and amino acid sequences of the entire human alpha-1 (III) collagen. A;Reference number: S04887; MUID:89386015; PMID:2780304

A; Accession: S04887

A;Molecule type: mRNA A;Residues: 149-163, 'G', 164-240,'D', 242-471,'D',473-487,'L',489,'S',491-613,'Y',615-634,' A;Cross-references: EMBL:X15332; NID:g29545; PIDN:CAA33387.1; PID:g930045 A;Note: the authors' translation of residues 905-932 is inconsistent with the nucleotide R;Seyer, J.M.; Kang, A.H.

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A,Title: Covalent structure of collagen: amino acid sequence of alphal (III)-CB9 from tyr
A,Reference number: A90446; MUID:81208139; PMID:7016180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Molecule type: protein
A; Molecule type: protein
A; Mesidues: 965-979; A', 1911-984, PS', 987, 'QN', 990-1096,'P', 1098-1152,'AT', 1155,'S', 1157-1
A; Experimental source: liver
R; Loidl, H.R.; Brinker, J.M.; May, M.; Pihlajaniemi, T.; Morrow, S.; Rosenbloom, J.; Myez
R; Loidl, H.R.; Brinker, J.M.; May, M.; Pihlajaniemi, T.; Morrow, S.; Rosenbloom, J.; Myez
A; Liele: Acids Ree: 12, 9838-9394, 1984
A; Title: Molecular cloning and carboxyl-propeptide analysis of human type III procollager
A; Reference number: A93551; MUID:85087944; PMID:6096827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1065-1155, 'P., 1157-1466 < LOI>
A; Cresidues: 1065-1155, 'P., 1157-1466 < LOI>
A; Cress-references: EMBL:X01655; EMBL:X01742; NID:g29584; PIDN:CAA25821.1
B; Miskulin, M.; Dalgleish, R.; Kluve-Beckerman, B.; Rennard, S.I.; Tolstoshev, P.; Brant]
Biochemistry 25, 1408-1413, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: translated from GB/EWBL/DDBJ
A;Status: translated from GB/EWBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: 161-1200 <MIS>
A;Molecule type: 161-1200 <MIS>
A;Cross-references: GB:MI3146; NID:g180415; PIDN:AAA52003.1; PID:g180416
B;Emanuel, B.S.; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C.
R;Emanuel, B.S.; Cannizzaro, L.A.; Sager, J.M.; Myers, J.C.
A;Title: Human alpha 1(III) and alpha 2(V) procollagen genes are located on the long arm A;Reference number: 159025; MUID:85216505; PMID:3858826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: the authors translated the codon TTC for residue 1057 as Tyr; the codons given for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Comment: Prolines and lysines at the third position of the tripeptide repeating unit (C 3-hydroxylated. About 15% of the lysines are 5-hydroxylated and some are subsequently O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Map position: 2431-2431
A,Introns: 27/1, 94/3; 111/3; 149/3; 176/3; 554/3; 587/3; 1175/3; 1275/1; 1337/3; 1418/3
A;Introns: 27/1, 94/3; 111/3; 149/3; 176/3; 554/3; 587/3; 1175/3; 1275/1; 1337/3; 1418/3
A;Note: the list of introns is incomplete; defects in this gene can result in Ehlers-Danl
C;Complex: type III collagen is a homotrimer of monomers initially linked by disulfide bc
er of their length, is formed with desmosine cross-links made from lysine and allysine re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Description: structural component of extracellular fibrous polymer that maintains integ C; Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; C; Keywords: coiled coil; Ehlers-Danlos syndrome; extracellular matrix; glycoprotein; hydis; F; 1-23, Domain: signal sequence #status predicted <SIG>
F; 24-153, Domain: amino-terminal propeptide #status predicted <PRO>
F; 19.190, Domain: von Willabrand factor type C repeat homology <VWC>
F; 154-121, Product: collagen alpha 1(III) chain #status predicted <MAT>
F; 154-167, Region: amino-terminal nonhelical telopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1176-1240,'V',1242-1356,'P',1358-1466 <CHU>
A;Cross-references: GB:M10615; GB:M10793; GB:M10794; GB:M10795; GB:M10796; GB:M10797; GB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Human type III collagen gene expression is coordinately modulated with the type A;Reference number: 152393; MUID:86187804; PMID:3754462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: mRNA
A,Residues: 1165-1196 <EMA>
A,Cross-references: GB:M11134; NID:g180417; PIDN:AAA52004.1; PID:g180418
R;Chu, M.L.; Weil, D.; de Wet, W.; Bernard, M.; Sippola, M.; Ramirez, F.
J. Biol. Chem. 260, 4357-4363, 1988
A,Title: Isolation of cDNA and genomic clones encoding human pro-alpha1(III)
A,Reference number: A92516; MUID:85157600; PMID:2579949
                                                                                             A;Molecule type: mRNA
A;Residues: 950-1018,'Y',1020-1183,'S',1185-1466 <MAN>
A;Cross-references: EMBL:X06700; NID:g30053; PIDN:CAA29886.1; PID:g30054
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F;1197-1221/Region: carboxyl-terminal nonhelical telopeptide
F;1222-1466/Domain: carboxyl-terminal propeptide #status predicted <CPR>F;1238-1466/Domain: fibrillar collagen carboxyl-terminal homology <PCC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Cross-references: GDB:118729; OMIM:120180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                  R;Seyer, J.M.; Kang, A.H.
Biochemistry 20, 2621-2627, 1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source: liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Accession: I79359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A90446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: I52393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: A92516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: A93551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: GDB: COL3A1
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A.Residues: 186-194 «MIL>

A.Residues: 186-194 «MIL>

A.Residues: 186-194 «MIL>

A.Cross-references: GBS-62925; NID:g386425; PIDN:AAD13937.1; PID:g4261637

R.Chiodo, A.A.; Sillence, D.O.; Cole, W.G.; Bateman, J.F.

Biochem. J. 311, 939-943, 1995

A.Title: Abnormal type: III collagen produced by an exon-17-skipping mutation of the COL3

A.Reference number: S59511; MUD:96067614; PMID:1487954

A.Accession: S5951

A.Residues: 302-423 «CHI>

A.Residues: 302-423 «CHI>

A.Residues: 302-423 «CHI>

A.Residues: 302-433 «CHI>

A.Residues: 302-4311, 1978

A.Title: Covalent structure of collagen: amino acid sequence of five consecutive CNBr pe

A.Title: Covalent structure of collagen: amino acid sequence of five consecutive CNBr pe

A.Residues: 399-675, N, 677-27 «SEY3>

A.Residues: 399-675, N, 677-27 «SEY3>

A.Residues: 399-675, N, 677-27 «SEY3>

A.Residues: 399-675, N, 677-27 «SEY3>

A.Residues: 399-675, N, 677-27 «SEY3>

A.Residues: 399-675, N, 677-27 «SEY3>

A.Residues: 399-675, N, 677-27 «SEY3>

A.Residues: 399-675, N, 677-27 «SEY3>

A.Residues: 399-675, N, 677-27 «SEY3>

A.Residues: 399-675, N, 677-27 «SEY3>

A.Residues: 399-675, N, 677-27 «SEY3>

A.Residues: 399-675, N, 677-27 «SEY3>

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A.Residues: 399-675, N, 677-27 «SEY3>

A.Residues: 399-675, N, 677-27 «SEY3>

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A.Residues: 399-675, N, 677-27 «SEY3>

A.Residues: 399-675, N, 677-27 «SEY3>

A.Residues: 399-675, N, 677-27 «SEY3>

A.Residues: 399-675, N, 677-27 «SEY3>

A.Residues: 399-675, N, 677-27 «SEY3>

A.Residues: 399-675, N, 677-27 «SEY3>

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A.Residues: 399-675, N, 677-27 «SEY3>

A.Residues: 399-675, N, 677-27 «SEY3>

A.Residues: 399-675, N, 677-27 «SEY3>

A.Residues: 399-675, N, 677-27 «SEY3>

A.Residues: 399-675, N, 677-27 «SEY3>

A.Residues: 399-675, N, 677-27 «SEY3>

A.Residues: 399-675, N, 677-27 «SEY3>

A.Residues: 399-675, N, 677-27 «SEY3>

A.Residu
Biochemistry 16, 1158-1164, 1977

A.Title: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptide
A;Reference number: A90399; MUID:77134724; PMID:557335
A;Recession: A90399
A;Molecule type: protein
A;Residues: "V, 169-225,229-232,"P',234-292,"D',294-398 <SEY1>
A;Residues: "V',169-225,229-232,"P',234-292,"D',294-398 <SEY1>
A;Rote: sequence corrected by A94562; attachment of 2-0-alpha-D-glucosyl-O-beta-D-galact
R;Seyer, J.M.
submitted to the Atlas, December 1977
A;Reference number: A94562
A;Molecule type: protein
A;Reference number: A94562
A;Molecule type: protein
A;Residues: "V',169-225,229-277,"A',279-292,"D',294,"S',296-398 <SEY2>
A;Residues: "V',169-225,229-277,"A',279-292,"D',294,"S',296-398 <SEY2>
A;Residues: "V',169-225,229-277,"A',279-292,"D',294,"S',296-398 <SEY2>
A;Residues: "W',169-225,229-277,"A',279-292,"D',294,"S',296-398 <SEY2>
A;Residues: "W',169-225,229-277,"A',279-292,"D',294,"S',296-398 <SEY2>
A;Residues: "W',169-225,229-277,"A',279-292,"D',294,"S',296-398 <SEY2>
A;Rote: author submitted corrections to A90399
R;Milewicz, D.M.; Witz, A.M.; Smith, A.C.; Manchester, D.K.; Waldstein, G.; Byers, P.H.
Am. J. Hum. Genet: 53, 62-70, 1993
A;Title: Parental somatic and germ-line mosaicism for a multiexon deletion with unusual
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A; Residues: 537-605 < LEB>
A; Cross-references: GB=MS9312; NID:g180815; PIDN:AAA52041.1; PID:g180816
B; Covabent etype: DNA
A; Cross-references: GB=MS9312; NID:g180815; PIDN:AA52041.1; PID:g180816
B; Seyer, J.M.; Mainardi, C.; Kang, A.H.
Biochemistry 19, 1583-1589, 1980
A; Title: Covabent structure of collagen: amino acid sequence of alphal (III)-CB5 from ty
A; Reference number: A90438
A; Molecule type: protein
A; Residues: 728-895; A; 897-964 < SBY4>
A; Residues: 728-895; A; 897-964 < SBY4>
A; Residues: 728-895; A; Bp7-964 < SBY4>
A; Residues: 728-895; A; Bp7-964 < SBY4>
A; Residues: 128-895; A; Bp7-964 < SBY4>
A; Residues: 265, 17070-17077, 1990
A; Title: A base substitution at a splice site in the COL3A1 gene causes exon skipping an A; Reference number: A38303; MUD:91009133; PMID:2145268
A; Residues: 861-1015 < CCL>
A; Cross-references: GB:J05617; GB:MS5603; GB:MS9227; NID:g180878; PIDN:AABS9383.1; PID:g
A; Note: a mutant sequence with 942-977 spliced out from a patient with Ehlers-Danlos syn R; Mankco, B.S; Dalghal(III) collagen: CDNA sequence for the 3' end.
A; Reference number: S02119; MUD:8189827; PMID:3357782
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A; Accession: 151868
A; Status: preliminary; translated from GB/EMBL/DDBJ
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C;Accession: S14998
R;Goping, I.S.; Frappier, J.R.H.; Walden, D.B.; Atkinson, B.G.
Plant Mol. Biol. 16, 699-711, 1991
A;Title: Sequence, identification and characterization of cDNAs encoding two different me A;Reference number: S14999
A;Reference number: S14997; MUID:91329703; PMID:1714322
A;Residues: 1-161 <GOP>
A;Residues: 1-161 <GOP>
C;Genetics:
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A; Residues: 1-866,'G',868-1464 <TOA>
A; Cross-references: ENGL:X22046, NID:9575321; PIDN:CAA36279.1; PID:9575322
R; Metsaeranta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E.
Biochim. Biophys. Acta 1089, 241-243, 1991
A; Title: Specific hybridization probes for mouse type I, II, III and IX collagen mRNAs.
A; Reference number: $16176; MUID:91274355; PMID:2054384
A; Accession: $16373
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Aug-1999
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Pred. No. 0.23;
2; Mismatches 0; Indels
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80.0%; Pred. No. 5.5;
ive 1; Mismatches
                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, November 1994 A;Reference number: S62120 A;Accession: S62120
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C.Superfamily: alpha-crystallin
C.Keywords: heat shock; Btress-induced protein
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                                                                     A;Molecule type: DNA
A;Residues: 1-1464 <TOM>
A;Cross-references: EMBL:X52046
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F;24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted F;153-154/Cleavage site: Pro-Gln (procollagen N-endopeptidase) #status predicted F;154/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted F;161,1212/Modified site: allysine (Lys) #status predicted F;263,284,860,977,1106/Modified site: 5-hydroxylysine (Lys) #status experimental F;263/Binding site: carbohydrate (Lys) (covalent) #status experimental F;584,1094/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental F;948-949/Cleavage site: Gly-Ile (Collagenase) #status experimental F;948-949/Cleavage site: Gly-Ile (Collagenase) #status experimental F;1106/Binding site: carbohydrate (Lys) (covalent) #status predicted
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Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cipate: 10-Apr-1996 #sequence revision 19-Apr-1996 #text_change 13-Aug-1999
CiAccession: S59856, S62120; S16373
R;Toman, P.D.; de Crombrugghe, B.
R;Toman, P.D.; de Crombrugghe, B.
A;Title: The mouse type-II procollagen-encoding gene: genomic cloning and complete DNA A;Reference number: S59856; MUID:95011609; PMID:7926795
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Csuperfamily: collagem alpha 1(1) chain; fibrillar collagem carboxyl-terminal homology;
C;Keywords: colled coll; extracellular matrix; glycoprotein; trimer; triple helix
F;408-636/Domain: fibrillar collagem carboxyl-terminal homology <FCC>
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Cyspecies: Rattus norvegicus (Norway rat)
Cydcession: 341067; A29905; S31924
Cydcession: S41067; A29905; S31924
Rydlumoff, V.; Maekelae, V.K.; Vuorio, E.
Biochim. Biophys. Acta 1217, 41-48, 1994
A;Ritle: Cloning of cDNA for rat pro alpha-1(III) collagen mRNA. Different expression ]
A;Reference number: S41067; MUID:94114571; PMID:8286415
A;Scatus: preliminary
A;Status: preliminary
A;Residues: 1-636 <GLUD>
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R;Frankel, F.R.; Hsu, C.Y.J.; Myers, J.C.; Lin, E.; Lyttle, C.R.; Komm, B.; Mohn, K.
DNA 7, 347-354, 1988
A;Title: Regulation of alpha-2 (I), alpha-1 (III), and alpha-2 (V) collagen mRNAs by eA;Reference number: A29905; MUID:88296083; PMID:2456904
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A,Residues: 308-482 <PRA>,
A,Cross-references: GB:M21354; NID:g203500; PIDN:AAA40942.1; PID:g203501
R,Glumoff, V: Maekelae, J.K.; Vuorio, E.
submitted to the EMBL Data Library, February 1993
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llarity 83.3%; Pred. No. 0.11;
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 2-636 <GL2>
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R; Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahi awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K. B. A; Hitle: G. 83-1101, 1999
A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyn. A; Reference number: A72456; MUID:99310339; PMID:10382966
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Cyacte: O's Decripy) #sequence_revision Us-Decripy) #text_change 15-Oct-1999
Cyactession: F69732
R;Kunst, R:, Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertert C.; Broulllet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chos A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, X.; Fuma, S.; Galizzi, A.; Gallert iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Fuma, S.; Galizzi, A.; Gallert iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y.; M.; Ogawa, K.; Ogiwara, A.; Darro, V.; Pohl, T.M.; Portetelle, Y.; Rieger, M.; Rivolta, C.; Rocha, B.; Rose, M.; Sekiguchi, J.; Sekowska, A.; Seror, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror, A; Authors: Voshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Tutle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: A69580; MUID:98044033; PMID:9384377
A; Accession: R69732
A; Status: Preliminary; nucleic acid sequence not shown; translation not shown
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A;Residues: 1-132 < xCUD.
A;Cross-references: GB:Z99110; GB:AL009126; NID:g2633472; PIDN:CAB13125.1; PID:e1183288;
A;Experimental source: strain 168
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                                           A;Molecule type: DNA
A;Residues: 1-209 «KUR»
A;Ctoss-references: GB:AE007870; PIDN:AAK89941.1; PID:g15159896; GSPDB:GN00170
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
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5
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Pred. No. 15;
1; Mismatches
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80.0%; Pred. No. 38;
iive 0; Mismatches
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A, Map position: linear chromoscme
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Best Local Similarity 72...
Best Local 8; Conservative
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Best Local Similarity 80.0
Matches 8; Conservative
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A; Residues: 1-383 < KAW>
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C;Accession: F70863
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Cole, S.T.; Brosch, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Atle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MulD:98295987; PMID:9634230
A;Status: Preliminary; nucleic acid sequence not shown; translation not shown A;Residues: 1-487 <COL>
A;Coss-references: GB:AL021246; GB:AL123456; NID:93261507; PIDN:CAA16024.1; PID:e123757 A;Benetican source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arylesterase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AE2981
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
R;Wood, D.W.; Setubal, Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
KATP, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C)Accession: C1501 msquence_revision 22-OCC-2001 #text_change 18-NOV-2002

R)Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUD:21608551; PMID:11743194

A;Status: preliminary
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CSB.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
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Gaps

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67.7%; Score 42; DB 2; Length 209; llarity 72.7%; Pred. No. 15; Conservative 1; Mismatches 2; Indels

147

137 VAGPGGEPAGG

a

1 IAGIGGEKAGG 11

Local Similarity hes 8; Conserv

Query Match

A;Gene: ada A;Map position: linear chromosome

C;Genetics:

A;Reaidues: 1-209 <KUR> A;Cross-references: GB:AE008689; PIDN:AAL44267.1; PID:g17741852; GSPDB:GN00187 A;Experimental source: strain CS8 (Dupont)

A;Status: preliminary A; Molecule type: DNA A,Accession: AE2981

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Gaps

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1; Indels

Score 44; DB 2; Length 487; Pred. No. 15; 0; Mismatches 1; Indels

71.0%; 90.0%;

Conservative

209 iAGIAGEKAG 218

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1 IAGIGGEKAG 10

C; Superfamily: folylpolyglutamate synthase

A; Gene:

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CjAccession: E95286
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse Stannett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse Stannan, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.; Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9889, 2001
A;Tible: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti A;Reference number: A95262; MUD:21396509; PMID:11481432
A;Accession: E95286
                                                                                                                                                                             A)Cross-references: GB:AB000916; GB:AB000666; NID:g2622674; PIDN:AAB86032.1; PID:g262268(
A)Experimental source: strain Delta H
C;Genetics:
A;Genetics: MTH1558
C;Superfamily: formylmethanofuran dehydrogenase chain C
C;Superfamily: formylmethanofuran metalloprotein; oxidoreductase; tungsten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Methanobacterium thermoautotrophicum
C.Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 20-Jun-2000
C.Accession: S63546; S57457
R.Hochheimer, A.; Schmitz, R.A.; Thauer, R.K.; Hedderich, R.
Bur. J. Blochem. 234, 910-920, 1995
A;Title: The tungsten formylmethanofuran dehydrogenase from Methanobacterium thermoautots
A;Reference number: S63519; MUID:96163477; PMID:8875452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Complex: heterotetramer of A (see PIR:S57456), B (see PIR:S57458), C, and D (see PIR:S5 C;Superfamily: formylmethanofuran dehydrogenase chain C C;Keywords: heterotetramer; iron-sulfur protein; metalloprotein; oxidoreductase; tungster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          formylmethanofuran dehydrogenase (EC 1.2.99.5) (tungsten) chain C - Methanobacterium them
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A; Residues: 1-298 «KUR»
A; Residues: 1-298 «KUR»
A; Cross-references: GB.AE006469; PIDN:AAK64855.1; PID:g14523269; GSPDB:GN00165
A; Experimental source: strain 1021, megaplasmid pSymA
R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein SMa0367 [imported] - Sinorhizobium meliloti (strain 1021)
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
                                                              A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-270 «HOCL»
A;Cross-references: EMBL:K87970; NID:g1890205; PIDN:CAA61214.1; PID:g1890211
A;Experimental source: strain Marburg, DSM 2133
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A; Reference number: A69000; MUID: 98037514; PMID: 9371463
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Pred. No. 40;
2; Mismatches
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Pred. No. 40;
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Best Local Similarity 63.6%;
Matches 7; Conservative
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Best Local Similarity 63.0
7; Conservative
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197 VARVGGEMAGG 207
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197 VARVGGEMAGG 207
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                                               A; Accession: H69074
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A;Residues: 1-1852 <GRA>
A;Crose-references: GB:M62554; GB:M37203; NID:g213049; PIDN:AAA49205.1; PID:g213050
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: glycoprotein; phosphoprotein; skeletal muscle; transmembrane protein
F;74-90/Domain: transmembrane #status predicted <TR01>
F;08-111/Domain: transmembrane #status predicted <TR02>
F;328-350/Domain: transmembrane #status predicted <TR05>
F;328-350/Domain: transmembrane #status predicted <TR05>
F;348-66/Domain: transmembrane #status predicted <TR09>
F;514-50/Domain: transmembrane #status predicted <TR09>
F;514-50/Domain: transmembrane #status predicted <TR09>
F;514-550/Domain: transmembrane #status predicted <TR09>
F;517-596/Domain: transmembrane #status predicted <TR19>
F;617-596/Domain: transmembrane #status predicted <TR11>
F;617-596/Domain: transmembrane #status predicted <TR12>
F;817-896/Domain: transmembrane #status predicted <TR13>
F;817-896/Domain: transmembrane #status predicted <TR13>
F;817-896/Domain: transmembrane #status predicted <TR13>
F;817-896/Domain: transmembrane #status predicted <TR13>
F;817-896/Domain: transmembrane #status predicted <TR13>
F;817-896/Domain: transmembrane #status predicted <TR13>
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C,Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Sep-1999
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F;1377-1402/Domain: transmembrane #status predicted <TR24>
F;1377-1402/Domain: transmembrane #status predicted <TR24>
F;99;102,274,470,813,115,71269,1485,1703,1713,1745,176,1760,1848/Binding site: carbohydrate F;407/Binding site: phosphate (Thr) (covalent) (by cAMP-dependent kinase) #status predic F;1471,1523,1738/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #st
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A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rigrapher, M.; Friedrich, K.; Knaus, H.G.; Striessnig, J.; Scheffauer, F.; Staudinger, Proc. Natl. Acad. Sci. U.S.A. 88, 727-731, 1991
A;Title: Calcium channels from Cyprinus carpio skeletal muscle.
A;Reference number: A37860; MUID:91126068; PMID:1846962
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R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, I. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           calcium channel protein alpha-1 chain, skeletal muscle - common carp C;Species: Cyprinus carpio (common carp)
C;Date: 31-May-1991 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: A37860
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                                                                                                                      Length 1332;
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66.7%; Pred. No. 1.6e+02;
ive 1; Mismatches 3; Indels
                                                                                                                                                                                                    1; Indels
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F;947-966/Domain: transmembrane #status predicted <TR17>
                                                                                                                          Score 41; DB 2;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: not compared with conceptual translation
                                                                                                                                                                                                    2; Mismatches
                                                                                                                          66.1%;
70.0%;
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                                                                                                                          Query Match 66.1
Best Local Similarity 70.0
Matches 7; Conservative
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469 VGGIGGEEAG 478
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Best Local S
Matches 8
               C;Genetics:
A;Gene: xkdO
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C.Species: Helicobacter pylori
A.Variety Errain J99
C.Species: train J99
C.Species: train J99
C.Species: L2-seb-1999 #sequence_revision 12-Feb-1999 #text_change 18-Aug-2000
C.SAccession: H71943
F.Species: L2-K-1999 #sequence_revision 12-Feb-1999 #text_change 18-Aug-2000
C.SAccession: H71943
F.Species: L2-K-1999
Mary L2-K-1999
Mature 397, 176-180, 1999
A.Titles: Genomic sequence comparison of two unrelated isolates of the human gastric path A.Reference number: A71800; MUID:99120557; PMID:9923682
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A;Residues: 1-438 <ARN>
A;Crestences: 1-438 <ARN>
A;Crestences: GB:AE001470; GB:AE001439; NID:G4154869; PIDN:AAD05927.1; PID:G415487
A;Experimental source: strain J99
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUD:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
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C64654
conserved hypothetical secreted protein HP1075 - Helicobacter pylori (strain 26695)
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64.5%; Score 40; DB 2; Length 298;
Best Local Similarity 88.9%; Pred. No. 43;
Matches 8; Conservative 0; Mismatches 1; Indels
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1 IAGIGGEKAGGF 12

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42 LAGIQGDEPGGF 53
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Search completed: September 18, 2004, 04:30:54 Job time : 15.5882 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 18, 2004, 03:48:54; Search time 8.94118 Seconds (without alignments) 69.884 Million cell updates/sec Run on:

US-10-615-959-43 62 1 IAGIGGEKAGGF 12 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		₩			SUMMAKIES	
Result		Query				
No.	Score	Match	Length	DB	ID	Description
г	62		ᅥ	7	CA13 HUMAN	P02461 homo sapien
7	58	93.5	636	Н	CA13_RAT	rattu
n	58	93.5	1464	Т	CA13_MOUSE	PO8121 mus musculu
4	44	71.0	191		HS21_MAIZE	P24631 zea mays (m
ហ	41	66.1	1332	П	XKDO_BACSU	
9	41	66.1	1852	٠.	CCAS_CYPCA	
7	40	64.5	270		FWDC_METTH	
80	40	64.5	270	Н	FWDC_METTM	Q59579 methanobact
D	40	64.5	383		DNAJ_PORGI	
10	39	62.9	175		YOCA_CAEEL	
11	39	62.9	354		RF1_LEPIN	
12	39	62.9	378		CSP_PLACL	
13	39	62.9	399		HXAA MOUSE	
14	39	62.9	1679	٦	FUR2_DROME	
15	38	61.3	267	Н	MTRC_METAC	Q8tu01 methanosarc
16	38	61.3	400	Н	LEUK HUMAN	
17	38	61.3	423	Н	TBX2_CAEEL	Q19691 caenorhabdi
18	38	61.3	495	-	AMPA_PSEAE	
19	38	61.3	592	Н	RB56 HUMAN	
20	37	59.7	62	Н	LAFX_LACJO	
21	37	59.7	198	-1	FLIN_RHIME	O54245 rhizobium m
22	37	59.7	232	Н	SSB_COREF	
23	37	59.7	269	г	POLG_PWVMI	
24	37	59.7	371	Н	TRMU_YERPE	
25	37	59.7	384	Н	GRP1_PETHY	
56	37	59.7	388	Н	NAH3_METJA	
27	37	59.7	422	7	VDR_XENLA	• •
28	37	59.7	462	٦	TRPE THETH	œ
29	37	59.7	468	٦	IL9R_MOUSE	Q01114 mus musculu
30	37	59.7	471	Н	K1CN_HUMAN	
31	37	59.7	486	-	XYLG_PSEPU	P23105 pseudomonas
32	37	59.7	499	П	DLDH_YEAST	
33	37	59.7	262	7	NPRM_BACME	Q00891 bacillus me

Q92319 mus musculu P34300 caenorhabdi P15417 bacteriopha P87124 schizosacch Q8xv18 ralstonia s O74031 methanobact Q48943 methanosarc Q8ker7 chlorobium Q8rd4 thermoanaer Q9rm20 helicobacte P55998 helicobacte Q55998 helicobacte	
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# ALIGNMENTS

RESULT 1 CA13 HUMAN CA13 HUMAN CA13 HUMAN CA13 HUMAN CA13 HUMAN COLOR CO
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VARIANT THR-698 Pope F.M. J. Med. VARIANT SEQUENCE OF 1176-1466 FROM N.A.
MEDINE=81157600; PubMed=257949;
Chu M.-L., Weil D., de Wet W.J., Bernard M.P., Sippola M., Ramirez F.;
"Isolation of cDNA and genomic clones encoding human pro-alpha 1
"Isolation Partial characterization of the 3' end region of the SEQUENCE OF 1065-1466 FROM N.A. MEDLINE=85087944; PubMed=6096827; Loidl H.R., Brinker J.M., May M., Pihlajaniemi T., Morrow S., Rosenbloom J., Myers J.C.; "Molecular cloning and carboxyl-propeptide analysis of human type III REVIEW ON VARIANTS.
MEDIJINE=97255959; PubMed=9101290;
Kuivaniemi H., Tromp G., Prockop D.J.;
Kuivaniemi H., Tromp G., Prockop D.J.;
Whutations in filtilar collagens (types I, II, III, and XI), fibrilassociated collagen (type IX), and network-forming collagen (type X) cause a spectrum of diseages of bone, cartilage, and blood vessels."; Toman D., Ricca G., de Crombrugghe B.;
"Nucleotide sequence of a cDNA coding for the amino-terminal region of human prepro alpha 1(III) collagen.";
Nucleic Acids Res. 16:7201-7201(1988). MEDLINE=93299988; PubMed=8514866; Tromp G., Wu Y., Prockop D.J., Madhatheri S.L., Kleinert C., Earley J.J., Zhuang J., Noerrgaard O., Darling R.C., Abbott W.M., Cole C.W., Jaakkola P., Rynaenen M., Pearce W.H., Yao J.S.T., Majamaa K., Smullens S.N., Gatalica Z., Ferrell R.E., Jimenez S.A., MEDLINE-86187804; PubMed-3754462; Miskulin M., Dalgleish R., Kluve-Beckerman B., Rennard S.I., Tolstoshev P., Brantly M., Crystal R.G.; "Human type III collagen gene expression is coordinately modulated with the type I collagen genes during fibroblast growth."; Biochemistry 25:1408-1413(1986). [7]
MEDINE=88189827, PubMed=3357782;
MEDINE=88189827, PubMed=3157782;
Mankoo B.S., Dalgleish R.;
Mankoo B.S., Dalgleish R.;
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MEDLINE-81208139; PubMed=7016180;
Seyer J.M., Kang A.H.;
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MEDLINE=89378752; PubMed=2777083;
Benson-Chanda V., Su M.W., Weil D., Chu M.-L., Ramirez F.;
"Cloning and analysis of the 5' portion of the human type-III
procollagen gene (COL3AI).";
Gene 78:255-265(1989). VARIANT AORTIC ANEURYSM ARG-303, AND VARIANT THR-668. 1(III)-CB9 from type III collagen of human liver."; Biochemistry 20:2621-2627(1981). MEDLINE-89098346; PubMed=3211760; Molyneux K., Dalgleish R.; "Human type III collagen 'variant' is a Nucleic Acids Res. 16:11833-11833 (1988) Nucleic Acids Res. 12:9383-9394(1984). Biol. Chem. 260:4357-4363(1985). MEDLINE=88303360; PubMed=3405773; SEQUENCE OF 1161-1200 FROM N.A. Mutat. 9:300-315(1997). SEQUENCE OF 1-170 FROM N.A. REVISION TO 1184. rissum=Placenta; procollagen." gene. 

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MEDLINE=91056145; PubMed=2243125; Rontusaari S., Trookop D.J.; Rontusaari S., Troom G., Kuivaniemi H., Romanic A.M., Prockop D.J.; "A mutation in the gene for type III procollagen (COL3A1) in a family with aortic aneurysms.";
                                                     mutations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               converts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tromp G., de Paepe A., Nuytinck L., Madhatheri S.L., Kuivaniemi H., "Substitution of valine for glycine 793 in type III procollagen in EMlers-Danlos syndrome type IV.", Hum. Mutat. 5:179-181(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Richards A.J., Narcisi P., Lloyd J.C., Ferguson C., Pope F.M., "The substitution of glycine 661 by arginine in type III collagen produces mutant molecules with different thermal stabilities and
                                                                                                                                                                                                                                                                                                            MEDLINE=91045136; PubMed=2235526; Zafarullah K., Kleinert C., Tromp G., Kuivaniemi H., Kontusaari Shu Y., Ganguly A., Prockop D.J.; Mu Y., Ganguly A., Prockop D.J.; G. To A polymorphism in exon 31 of the COL3Al gene."; Nucleic Acids Res. 18:6180-6180(1990).
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Richards A.J., Ward P.N., Narcisi P., Nicholls A.C., Lloyd J.C.,
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Jackson C.E., Michels V.V., Kaye M., Kuivaniemi H.; "Sequencing of cDNA from 50 unrelated patients reveals that in the trible-helical domain of type III procollagen are an infrequent cause of aortic aneurysms."; J. Clin. Invest. 91:2539-2545(1993).
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MEDLINE=93022543; Pubmed=1357232;
Johnson P.H., Richards A.J., Pope F.M., Hopkinson D.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT EDS-IV ARG-828.
MEDLINE=94016385; PubMed=8411057;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genet. 30:690-693(1993)
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REALINE-88296083; PubMed-2456904;
Reankel F.R., Hav C.-Y.J., Meyers J.C., Lin E., Lyttle C.R.,
Roam B., Mohn K.;
The stradiol in the immature rat uterus.";
The stradiol in the immature rat uterus.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CALTA RAT STANDARD; PRT; 636 AA.
P13941; 070604;
D1-JAN-1990 (Rel. 13, Created)
O1-JAN-1999 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Collagen alpha 1(III) chain (Fragment).
Collagen alpha 1(III) chain (Fragment).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94114571; PubMed=8286415; Glumoff V., Maekelae J.K., Vuorio B.; Cloning of cDNA for rat pro alpha 1(III) collagen mRNA. Different cloning of cDNA for rat pro alpha 1(III) collagen and fibronectin genes in experimental granulation tissue."; Biochim. Biophys. Acta 1217:41-48(1994).
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                                               Query Match 100.0%; Score 62; DB 1; Length 1466; Best Local Similarity 100.0%; Pred. No. 0.032; Matches 12; Conservative 0; Mismatches 0; Indels 0
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Wurtz T., Ellerstroem C., Lundmark C., Christersson C.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
InterPro; IPR008185; Fib_collagen.
InterPro; IPR00181; Fibzinogen_C.
InterPro; IPR01007; VWF.C.
Pfam; PF01410; COLFI; 1.
Pfam; PF01391; Collagen; 6.
ProDom; PD000007; Clg helix; 1.
ProDom; PD002078; Fib_collagen_C; 1.
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STRAIN-C57BL/6; TISSUE-Brain;

STRAIN-C57BL/6; TISSUE-Brain;

A Straubberg R.D., Feingold B.A., Grouse L.H., Derge J.G.,

A Leschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Leschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Leschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Leschlan S.F., Jordan H., Moore T., Mang J., Haich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldow M.F., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshkyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., McKernan K.J., Malek J.A., Gunaratne P.H.,

R. Richards S., Worley K.C., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rhich M.M. Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length
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MEDLINE=95011609; PubMed=7926795;
Toman D., de Crombrugghe B.;
The mouse type-III procollagen-encoding gene: genomic cloning and complete DNA sequence.";
Gene 147:161-168(1994).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
SMART; SM00038; COLFI; 1.
PROSTER; PS01208; VWFC 1; PARTIAL.
Extracellular matrix, Connective tissue; Repeat; Hydroxylation;
Collagen; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                       .,
                                                                                                       COLLAGEN ALPHA 1(III) CHAIN.
CARBOXYL-TERMINAL PROPEFTIDE.
TRIPLE-HELICAL REGION.
NONHELICAL REGION (C-TERMINAL).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N -> D (IN REF. 2).
A -> G (IN REF. 2).
A -> G (IN REF. 2).
W, 61A48159F01D01EE CRC64;
                                                                                                                                                                                                                                                                                                                                        93.5%; Score 58; DB 1; Length 636; 83.3%; Pred. No. 0.066;
                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CA13 MOUSE STANDARD; PRT; 1464 AA. P08121; Q61429; Q9CRN7; 01-AUG-1988 (Rel. 08, Created) 15-UUG-199 (Rel. 38, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Collagen alpha 1(III) chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
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Wood L., Theriault N., Vogeli G.;
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                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 85...
Best Local 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              375 IAGVGGEKSGGF 386
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636 AA;
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SEQUENCE OF 810-1464 FROM N.A.

STRAIN=CSTBL/64): TISSUB=Embryonic head;

MATAN=CSTBL/64): TISSUB=Embryonic head;

MATAN=CSTBL/64): Albibata K., Yoshino M., Itoh M., Ishii Y.,

MATAWAN T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Azawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Azawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yammanka I.,

Asito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Satto R.,

Kadota K., Matsuda H.A., Ashburner M., Bancho S., Casawant T.,

Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schrim I., M., Staubli F., Suzuki R., Tomita M., Magner L., Mashio T.,

Sakai K., Okido T., Furuno M., Anon Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerte P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Toyo-oka K., Schoenbach C., Whittaker C., Whittaker C.,

Whynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

M. Washina-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collagen mRNAs.";
Biochim. Biophys. Acta 1089:241-243(1991).
-!-FUNCTION: Collagen type III occurs in most soft connective tissues along with type I collagen.
-!- SUBUNIT: Trimers of identical alpha 1(III) chains. The chains are linked to each other by interchain disulfide bonds. Trimers are also cross-linked via hydroxylysines.
-!- PIM: Proline residues at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: O-linked glycan consists of a Glc-Gal disaccharide bound to the oxygen atom of a post-translationally added hydroxyl group (By
"Complete nucleotide sequence of the N-terminal domains of the murine alpha-1 type-III collagen chain."; Gene 61:225-230(1987).
                                                                                        SEQUENCE OF 1-28 FROM N.A.
MEDIINE=85131189; PubMed=3972847;
Liau G., Mudryj M., de Crombrugghe B.;
"Identification of the promoter and first exon of the mouse alpha 1 (III) collagen gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metsaeranta M., Toman D., de Crombrugghe B., Vuorio E., "Specific hybridization probes for mouse type I, II, III and IX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
SIMILARITY: Contains 1 VWFC domain.
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EMBL; AK019448; BAB3Ī724.1; -.
EMBL; X57983; CAA41048.1; -.
                                                                                                                                                                                 II) collagen gene.";
Biol. Chem. 260:3773-3777(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91274355; PubMed=2054384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1442-1464 FROM N.A. STRAIN=C57BL/6;
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S59856; S59856.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC058724; AAH58724,
EMBL; M18933; AAA37338.1,
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PIR;
MGD;
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MEDLINE=91329703; PubMed=1714322;
Goping I.S., Frappier J.R.H., Walden D.B., Atkinson B.G.;
Goping I.S., identification and characterization of cDNAs encoding two different members of the 18 kDa heat shock family of Zea mays L.";
Plant Mol. Biol. 16:699-711(1991).
--- SUBCELLULAR LOCATION: Cytoplasmic.
--- SIMILARITY: Belongs to the small heat shock protein (HSP20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRIPLE-HELICAL REGION.
NOWHELICAL REGION (C-TERMINAL).
O-LINED (GAL. .) (BY SIMILARITY).
HYDROXYLATION (BY SIMILARITY).
HYDROXYLATION (BY SIMILARITY).
HYDROXYLATION (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
                                                                                                                                                                                                     Probom, PD002078; Fib_collagen_C; 1.
SMART; SM00018; COLFT; 1.
SMART; SM0014; VMC; 1.
SMART; PS01208; VWFC 1; 1.
PROSITE; PS50184; VWFC_1; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
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COLLAGEN ALPHA 1(III) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE.
WWFC.
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INTERCHAIN (BY SIMILARITY)
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01-MAR-1992 (Rel. 21, Last sequence update)
01-UND-1994 (Rel. 29, Last annotation update)
175 kDa class II heat shock protein.
Zea mays (Maize).
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2; Mismatches
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BY SIMILARITY.
InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
InterPro; IPR008165; Fib collagen_C.
InterPro; IPR002181; Fibrinogen_C.
InterPro; IPR001011; Fibrinogen_C.
InterPro; IPR01107; VWF_C.
Pfam; PF01410; ColF1; 11.
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                                                                                                                                                                             ProDom; PD000007; Clg helix; 1.
ProDom; PD002078; Fib_collagen_
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1203 IAGVGGEKSGGF 1214
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es 10; Conservative
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1196 119
1464 AA;
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1093
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SIGNAL
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Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
A Borriss R., Boureier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouilet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Choi S.K., Codani J.J., Fabret C., Farrari E., Foulger D.,
Chi S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
Guiseppi G., Guy B.J., Hajed K., Halech J., Harva M., Jones I.,
A Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones I.,
Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
A Mirita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
A Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
A Parro V., Pohl T.M., Porterelle D., Porwollik S., Prescott A.M.,
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Sakiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
A Sato T., Scanlan E., Schleich S., Schreeter R., Scoffene F.,
A Takeuchi M., Tanakoshi A., Tanaka T., Takenaru K.,
A Takeuchi M., Tanakoshi A., Tanaka T., Tarpetra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vanier F., Vassarotti A.,
Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPROuss,,,
Pfam; PF00011; HSP20; 1.
PROSITE; PS01031; HSP20; 1.
PROSITE; Bock; Multigene family.
Heat shock; Multigene family.
Heat Spock; Multigene family.
Heat Spock; Multigene family.
Heat Spock; Multigene family.
Heat Spock; Multigene family.
Heat Spock; Multigene family.
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01-0CT-1996 (Rel. 34, Last sequence update)
110-0CT-2003 (Rel. 42, Last annotation update)
NADO OR BSU12680.
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                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002068; Hsp20.
InterPro; IPR008978; HSP20_chap.
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MaizeDB; 51309; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agatoxin-IVA (onega-Aga-IVA). Calcium channels containing the alpha-1S subunit play an important role in excitation-contraction coupling in skeletal muscle (By similarity).

COMPLEXES, CONSISTING OF ALPHA-1, ALPHA-2, BETA AND DELTA SUBUNITSUBNIT A 1:1:1:1 RATIO. THE CHANNEL ACTIVITY IS DIRECTED BY THE PORRISC SUBUNIT IS SUFFICIENT TO GENERALE VOLTAGE-SENSITIVE CALCIUM

SUBUNIT IS SUFFICIENT TO GENERALE VOLTAGE-SENSITIVE CALCIUM
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyprinus carpio (Common carp).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprindae; Cyprinus.
NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Skeletal muscle;
MEDLINE=91126068; PubMed=1846962;
Grabher M., Friedrich K., Knaus H.-G., Striessnig J., Scheffauer F.,
Staudinger R., Koch W.J., Schwartz A., Glossmann H.;
"Calcium channels from Cyprinus carpio skeletal muscle.";
Proc. Natl. Acad. Sci. U.S., 88:727.31(1991).
-!- FUNCTION: Voltage-sensitive calcium channels (VSCC) mediate the entry of calcium ions into excitable cells and are also involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in a variety of calcium-dependent processes, including muscle contraction, gene expression, cell motility, cell division and cell death. The isoform alpha-1S gives rise to L-type calcium currents. Long-lasting (L-type) calcium channels belong to the "high-voltage activated" (HVA) group. They are blocked by dihydropyridines (DHP), phenylalkylamines, benzothiazepines, and B omega-agatoxin-IIIA (omega-aga-IIIA). They are however insensitive to omega-conotoxin-GVIA (omega-CTx-GVIA) and omega-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Dihydropyridine-sensitive L-type, skeletal muscle calcium channel
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                                                                                                                      -!- SIMILARITY: STRONG, TO B. SUBTILLS YOBO.
                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
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Pfam; PF01464; SLT; 1.
                                                                                                                                                                                                                                                                                                                                          EMBL, Z70177; CAA94037.1; -.
EMBL, Z99110; CAB13125.1; -.
PIR, F69732; F68732.
Subtiliat; BG11549; xkdo.
                                                                                                    Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 70.0
Matches 7; Conservative
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SEQUENCE 1332 AJ
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FWDC METTH O2760;
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                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
CHANNEL ACTIVITY. THE AUXILIARY SUBUNITS BETA AND ALPHA-2/DELTA LINKED BY A DISULFIDE BRIDGE REGULATE THE CHANNEL ACTIVITY. AN ADDITIONAL GAMMA SUBUNIT IS PRESENT ONLY IN SKELETAL MUSCLE L-TYPE CHANNEL (BY SIMILARITY).

SUBCELLULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: Skeletal muscle.

PTM: MAX NOT BE PHOSEPDORYJATED.

SIMILARITY: Belongs to the calcium channel alpha-1 subunits
                                                                                                                                                                                                                                                               PRINTS; PRO1634; LVDCCALPHAIS.

Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Calcium channel; Glycoprotein; Repeat; Multigene family; Calcium-binding; Phosphorylation.

REPEAT 57
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CYTOPLASMIC (POTENTIAL).
S5 OF REPEAT III.
EXTRACELLULAR (POTENTIAL)
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S5 OF REPEAT I.
EXTRACELLULAR (POTENTIAL)
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S2 OF REPEAT II.
CYTOPLASMIC (POTENTIAL).
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S4 OF REPEAT II.
CYTOPLASMIC (POTENTIAL).
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83 OF REPEAT III.
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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S1 OF REPEAT I.
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S1 OF REPEAT II.
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CYTOPLASMIC (POTENTIAL).
S1 OF REPEAT III.
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                                                                                                                                                                  PIR; A37860; A37860.
InterPro; IPR001682; Ca/Na_pore.
InterPro; IPR002011; Ca_channel_alpha.
InterPro; IPR002111; Cal_channel_Trph.
InterPro; IPR005821; Ion_trans.
InterPro; IPR005846; LVDCCAlpha1.
InterPro; IPR005840; LVDCCAlpha1.
InterPro; IPR00580; M+channel_nlg.
PRIMTS; PR001630; LVDCCALPHA1.
PRINTS; PR001630; LVDCCALPHA1.
                                                                                                                                                           EMBL; M62554; AAA49205.1; -.
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(BY SIMILARITY).

CALCIUM ION SELECTIVITY AND PERMEABILITY
(BY SIMILARITY).

CALCIUM ION SELECTIVITY AND PERMEABILITY
(BY SIMILARITY).

CALCIUM ION SELECTIVITY AND PERMEABILITY
(BY SIMILARITY).

DIHYDROPKEIDINES (BY SIMILARITY).

PHENYLALKYLAMINES (BY SIMILARITY).

BY SIMILARITY).
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STRAIN=Delta H;
MEDLINE=98037514; PubMed=9371463;
Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
                                                                                                                                                                                                                                                                                               CALCIUM ION SELECTIVITY AND PERMEABILITY
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2001 (Rel. 40, Last amnotation update)
Tungsten-containing formylmethanofuran dehydrogenase II subunit C (EC 1.2.99.5)
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Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
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                                                                               CITOLAGNIC (FOIENITAL).

S1 OF REPEAT IV.
S4 OF REPEAT IV.
CYPOLASHIC (FOTENTIAL).
S5 OF REPEAT IV.
EXTRACELLULAR (FOTENTIAL).
S6 OF REPEAT IV.
EXTRACELLULAR (FOTENTIAL).
S6 OF REPEAT IV.
POLY-GIY.
POLY-GIY.
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            CYTOPLASMIC (POTENTIAL).
S1 OF REPEAT IV.
EXTRACELLULAR (POTENTIAL)
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OF REPEAT III.
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Pred. No. 89;
1; Mismatches
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Conservative
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IAGVPTEKGGGF 175
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es 8; Conserv
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                                                                                                                                                                                                                                                                            PATHWAY: Methanogenesis, first step. SUBUNIT: THIS ENZYME IS COMPOSED OF SEVEN SUBUNITS FWDA (65 KDa), FWDB (53 KDa), FWDC (31 kDa), FWDD (15 kDa), FWDB, FWDF, AND FWDG. INDUCTION: By growth on tungsten or molybdenum under anaerobic
                                                                                                                                                                                                       CATALYTIC ACTIVITY: Formylmethanofuran + H(2)O + acceptor = CO(2) + methanofuran + reduced acceptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE00Usic, ....
PIR; H69074; H69074.
InterPro; IPR002493 UUT14.
Pfam; PF01493; GXGXG; 1.
Oxidoreductase; Tungsten; Methanogenesis; Repeat; Complete proteome. 7 X 13 AA REPEATS OF [GW] -X-X-M-X-X-G-nownTN 80 213 7 X 13 AA REPEATS OF [GW] -X-X-M-X-X-G-nownTN X-[IU] -X-[IU] -X-G.
                                                                                                                              J. Bacteriol. 179:7135-7155(1997).
-!- FUNCTION: CATALYZES THE REVERSIBLE OXIDATION OF CO(2) AND METHANOFURAN (MRR). TO N-FORMYLMETHANOFURAN (CHO-MFR). CAN ONLY OXIDISE FORMYLMETHANOFURAN. THIS ENZYME IS OXYGEN-LABILE.
Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum delth: functional analysis and comparative genomics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133)
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q59579; 008493; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last sannotation update) Tungsten-containing formylmethanofuran dehydrogenase II subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.5%; Score 40; DB 1; Length 270; 63.6%; Pred. No. 23; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96163477; PubMed=8575452;
Hochheimer A., Schmitz R.A., Thauer R.K., Hedderich R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     043A9FFBBA554D36 CRC64;
                                                                                                                                                                                                                                                             ENZYME REGULATION: Not inactivated by cyanide.
                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the fwdC/fmdC family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methanobacteriaceae; Methanothermobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28641 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 VARVGGEMAGG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IAGIGGEKAGG 11
                                                                                                                                                                                                                                           COFACTOR: Tungsten.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144
163
182
201
270 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=79929;
                                                                                                                                                                                                                                                                                                                                                     conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EC 1.2.99.5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
            thermoautotrophicum contains sequence motifs characteristic for enzymes containing molybdopterin dinucleotide.";

Eur. J. Biochem. 234:910-920(1995).

-!- FUNCTION: CATALYZES THE REVERSIBLE OXIDATION OF CO(2) AND METHANOFURAN (MFR. TO N. FORMYLMETHANOFURAN (CHO-MFR). CAN ONLY OXIDISE FORMYLMETHANOFURAN. THIS ENZYME IS OXYGEN-LABILE.

-!- CATALYTIC ACTIVITY: Formylmethanofuran + H(2)O + acceptor = CO(2)
                                                                                                                                                 -!- COFACTOR: Tungsten.
-!- PATHARY: Methanogenesis; first step.
-!- SUBUNIT: THIS ENZYME IS COMPOSED OF SEVEN SUBUNITS FWDA (65 kDa), FWDB (53 kDa), FWDC (31 kDa), FWDD (15 kDa), FWDE, FWDF, AND FWDG (BY SIMILARITY).
The tungsten formylmethanofuran dehydrogenase from Methanobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [GW]-X-X-M-X-X-G-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ross B.C., Barr I., Patterson M., Agius C., Rothel L., Margetts M.,
Hocking D., Webb E.;
                                                                                                                                                                                                                                      -!- INDUCTION: By growth on tungsten or molybdenum under anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Chaperone protein dnaJ (Immunoreactive heat shock protein dnaJ).
DNAJ OR PG1776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  romonas gingivalis polypeptides and nucleic acids."; ed (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E0A369D2ACFEC46F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X87970; CAAG1214.1; -.
EMBL; X87970; CAAG1214.1; -.
Pitar: Pro1493; GXGXG; 1.
Oxidoreductase; Tungsten; Methanogenesis; Repeat.
DOMAIN 80 213 7 X 13 AA REPRATS OF X-[IL]-X-[IV]-X-G.
                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the fwdC/fmdC family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.5%; Score 40; DB 1; 63.6%; Pred. No. 23; iive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          383 AA
                                                                                                                                     + methanofuran + reduced acceptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Porphyromonadaceae; Porphyromonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28554 MW;
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197 VARVGGEMAGG 207
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99
118
144
163
182
201
270 AA;
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                        conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=W50;
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REPEAT
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REPEAT
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STRAIN=W83;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

STATIS-56601 / Serogroup Icterohaemorrhagiae / Serovar lai;

STATIS-5661 / Serogroup Icterohaemorrhagiae / Serovar lai;

MEDLINE-22598143; PubMed=12712204;

A Ens S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,

A Lang Y.-X., Gu W.-Y., Zang Y.-Q., Zai Z., Sheng H.-Q., Jia J., Tu Y.-F.,

A Lang Y.-X., Gu W.-Y., Zang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,

A Lang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,

A Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,

A Unique physiological and pathogenic features of Leptospira

Interrogans revealed by whole-genome sequencing.";

Nature 422:888-893(2003).

-I-FUNCTION: Peptide chain release factor I directs the termination

of translation in response to the peptide chain termination codons

UAG and UAA (By similarity).

-I-SUMLEALULAR LOCATION: Cytoplesmic.

-I-SUMLARITY: Belongs to the prokaryotic/mitochondrial release
                                                                                                                               Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last nonotation update)
Hypothetical 19.4 kDa protein ZC395.10 in chromosome III.
                                                                                                                                                                                                                                                        Connell M.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 168 POLY-GLU.
175 AA; 19431 MW; D5C136F30446E37A CRC64;
                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Belongs to the p23 / wos2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.9%; Score 39; DB 1; 72.7%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Peptide chain release factor 1 (RF-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASP/GLU-RICH.
                                                                                                                                                   Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; T27543; T27543.
WormPep; ZC395.10; CE01436.
InterPro; IPR008978; HSP20_chap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U13642; AAG00038.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 AGIGGGMANGF 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AGIGGEKAGGF 12
                                                                                                       Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                    STRAIN=Bristol N2;
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                         NCBI_TaxID=6239;
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Q8F9S6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                        ZC395.10
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RF1_LEPIN
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                                                                                                                                          Porphyronogas graduates of the Orla paragonic parterium.

J. Bacteriol. 185:5591-5601(2003).

-!- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpB, the ATPase activity of dnaK (By similarity).

-!- COFACTOR: Binds 2 zinc ions per monomer (By similarity).

-!- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).

-!- SUMILARITY: Belongs to the dnaJ family.

-!- SIMILARITY: Contains 1 J domain.

-!- SIMILARITY: Contains 1 CR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00636; DNAJ 1; 1.
PROSITE; PS50076; DNAJ 2; 1.
PROSITE; PS00637; DNAJ CXXCXGXG; FALSE NEG.
Chaperone; DNA replication; Heat shock; Repeat; Zinc; Metal-binding;
MEDLINE=22829867; PubMed=12949112; Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E., Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M., Haft D.H., Kolonay J.F., Nelson W.C., Mason T., Tallon L., Gray J., Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J., Dewhirst F.B., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ő
                                                                                                                         Complete genome sequence of the oral pathogenic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 383;
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ZINC 1 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 2 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
ZINC 1 (BY SIMILARITY).
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CXXCXGXG MOTIF.
CXXCXGXG MOTIF.
CXXCXGXG MOTIF.
CXXCXGXG MOTIF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J-DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002939; DnaJ C.
InterPro; IPR001305; DnaJ CXXCXGXG.
InterPro; IPR001623; DnaJ N.
InterPro; IPR008971; HSP40 DnaJ pep.
InterPro; IPR003095; HSP_DnaJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Pfam; PF01556; DnaJ; 1.
Pfam; PF01684; DnaJ C; 1.
PRINTS; PR00625; DNAJPROTEIN.
SWART; SM00271; DnaJ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF145797; AAD39493.1; -.
EMBL; AE017178; AAQ66777.1; -.
HSSP; P08622; 1XBL.
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Best Local Similarity 63.0
7; Conservative
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124
1124
1161
127
127
1171
1174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 383 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome.
DOMAIN 6
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Q23280;
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TIGR;

REPEAT

METAL

YOCA\_CAEEL RESULT 10

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Gaps

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Indels

Length 175;

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                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- MISCELLANEOUS: The circumsporozoite protein is the immunodominant surface antigen on the sporozoite (the infective stage of the malaria parasite that is transmitted from the mosquito to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -I- MISCELLANEOUS: The C-terminal region is probably used for anchoring the procein to the cell membrane. The repeat sequences would be the surface antigen of the organism.
-!- SIMILARITY: Contains I TSP type-I domain.
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=87102878; PubMed=3802196;
Galinski M.R., Arnot D.E., Cochrane A.H., Barnwell J.W.,
Nussenzweig R.S., Enea V.;
"The circumsporozoite gene of the Plasmodium cynomolgi complex.";
Cell 48:311-319(1987).
                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                         62.9%; Score 39; DB 1; Length 354; 72.7%; Pred. No. 42; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                         Pfam; PF004/2; kr-1, ...
TIGREPMS; TIGROUNS; prfA; 1.
PROSITE; PS00745; RF PROK I; 1.
Protein biosynthesis; Complete proteome.
Protein a new Ann. 40099 MW; 779A91ACCC997A59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
17-Cummsporzeoite protein precursor (CS).
Plasmodium cynomolgi (strain London).
                                                                                                                                                   HAMAP; MF_00093; -; 1.
InterPro, IPR005139; PCRF.
InterPro; IPR000352; Pep rel_factor_I.
InterPro; IPR004373; PrfĀ.
Pfam; PF03462; PCRF; 1.
Pfam; PF00472; RF-1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M15101; AAA29537.1; -.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam, PF00090; tsp 1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
                                                                                                                                      EMBL; AE011202; AAN47313.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50092; TSP1; 1.
                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 72..
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                           113 AGTGGEEAGLF 123
                                                                                                                                                                                                                                                                                                                                                                2 AGIGGEKAGGF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vertebrate host)
factor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=5831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLACL
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1-14.
1-15.
1-16.
1-17.
1 x 11 AA TANDEM REPEATS OF G-N-[QR]-
[AE]-G-G-Q-A-G-A-G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Benson G.V., Nguyen T.-H.E., Maas R.L.;
"The expression pattern of the murine Hoxa-10 gene and the sequence recognition of its homeodomain reveal specific properties of Abdominal B-like genes."
Mol. Cell. Biol. 15:1591-1601(1995).
                   CIRCUMSPOROZOITE PROTEIN.
18 X 6 AA TANDEM REPEATS OF D-G-A-R-A-
[EA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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0
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MEDLINE=92073356; PubMed=1683707;
Singh G., Kaur S., Stock J.L., Jenkins N.A., Gilbert D.J.,
Copeland N.G., Potter S.S.;
"Identification of 10 murine homeobox genes.";
Proc. Natl. Acad. Sci. U.S.A. 88:10706-10710(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.9%; Score 39; DB 1; Length 378; 70.0%; Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     TSP TYPE-1.
8295A913C36420C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-07U-1993 (Rel. 26, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Homeobox protein Hox-Al0 (Hox-1.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      399 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                PROBABLE.
 Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=CD-1; TISSUE=Kidney;
MEDLINE=95166244; PubMed=7862151;
                                                                                                                         .5.
                                                                                                                                                                  -8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    37462 MW;
Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 AGAGGNRAGG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AGIGGEKAGG 11
 Malaria; Sporozoite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                     304
378 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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1123
1123
1129
1135
1141
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1153
1153
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189
195
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212
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SEQUENCE
                          CHAIN
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REPEAT
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                SIGNAL
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P30432; Q24301;
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                                                                                                                                                                                                                                                                           ISOId=P31310-2; Sequence=VSP 002386, VSP 002387;
TISSUB SPECIFICITY: EXPRESSED IN THE DEVELOPING LIMB BUD WHERE IT
IS RESTRICTED TO THE MESENCHYME ALONG THE PROXIMAL-DISTAL AXIS.
ALSO FOUND IN DEVELOPING GUT AND URCGENITAL TRACT. IN ADULT
TISSUE, BOTH FORMS FOUND IN KIDNEY BUT ONLY ISOFORM 1 IS EXPRESSED
                                               Murtha M.T., Leckman J.F., Ruddle F.H.;
"Detection of homeobox genes in development and evolution.";
Proc. Natl. Acad. Sci. U.S.A. 88:10711-10715(1991).
-!- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
                                                                                                                                                                                                                                                                                                                                                                                   DEVELOPMENTAL STAGE: EMBRYONIC EXPRESSION INCREASES FROM DAY 9 TO DAY 12 AND THEN DECLINES TO DAY 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00046; homeobox; 1.

PRINTS; PR00024; HOMEOBOX.

ProDown, PD0000010; Homeobox; 1.

SMART; SM01389; HOX; 1.

PROSITE; PS00027; HOMEOBOX 1; 1.

PROSITE; PS00027; HOMEOBOX 2; 1.

Homeobox; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39; DB 1; Length 399; Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /FIId=VSP 002386.
DSL -> MCQ (in isoform 2)
/FIId=VSP 002387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7529624FC6057042 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Belongs to the Abd-B homeobox family.
                                                                                                                                                     BINDS TO THE DNA SEQUENCE 5'-AA[AT]TTTTATTAC-3'.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (in isoform 2).
                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Iranscription regulation; Alternative splicing.
DOMAIN 26 38 GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-GLY.
GLN/PRO-RICH.
                                                                                                                                                                                                                                            IsoId=P31310-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLY-GLY.
POLY-GLY.
HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Missing
SEQUENCE OF 346-370 FROM N.A.
STRAIN=C57BL/6; TISSUE=Spleen;
MEDLINE=92073357; PubMed=1720547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P0283; 9ANT.
TRANSFAC; T0115; -.
ID10; MGI:96171; Hoxal0.
InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      399 AA; 41415 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L08757; AAA67125.1; -. EMBL; M81659; AAA63312.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 70.0
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                   IN SKELETAL MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; 149754; 149754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306
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RA MEDINE-20196006; PUNDMEG-10/31132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Abrial J.E., Rogers Y.-H.C., Blazej R.G., Champe M., Pétélfére B.D.,

RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Beson K.Y. Bearn B.P., Bhandari D., Bolshakov S.,

RA Burkis K.C., Busam D.A., Buttler H., Cadieu E., Center A., Chandra I.,

RA Burkis K.C., Busam D.A., Buttler H., Cadieu E., Center A., Chandra I.,

RA Burkis K.C., Busam D.A., Buttler H., Cadieu E., Center A., Chandra I.,

RA Burkis K.C., Busam D.A., Buttler H., Cadieu E., Center A., Chandra I.,

RA Burkis K.C., Busam D.A., Bulman T.J., Wain M.O. Bases S.,

RA Godson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Cadbielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Dodson K., Cong F. Gorrell J.H., Gu Z., Guan P., Harris M.

RA Jali M., Harvey D.A., Heiman T.J., Wei M.-H., Ilbegwam C.,

A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,

Luk M., Murkhy B., Murphy L., Muzny D.M., Nelson D.L.,

Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Balazzolo M., Pattenan G.S., Pan S., Pollard J., Puri, Wang A.H.,

Ra Balazzolo M., Pattenan G.S., Pan S., Pollard J., Puri, Wang X.,

Ra Balazzolo M., Pattenan G.S., Pan S., Pollard J., Puri, Wang X.,

Ra Spier E., Spradling A.C., Stapleton M., Stupski M.P., San H.,

Spier E., Spradling A.C., Stapleton M., Stupski M.P., San B.,

A Hariskas R., Woodsey T., Wasaraman D.A., Weilssenbach J.,

Williams S.M., Woodsey T., Wasaraman D.A., Weilssenbach J.,

Walliams S.W., Woodsey T., Wasaraman D.A., Weilswick M. Wang G. Zhoo Q., Zhu X., San H. H.O.,

Ra Jahear X., Roger C., Stapleton M., Stupski M.P., San B., San B.,

Rabber R., Sc
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SERAIM=Cregon.R. Tuebingen, and Iso-1;
MEDLINE=92381036, PubMed=1512259;
MEDLINE=92381036, PubMed=1512259;
Rebirock A.J.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dumke U.,
Rehtrop M., Gateff E.A.F., Leunissen J.A.M., van de Ven W.J.M.;
"Cloning and functional expression of Dfurin2, a subtilisin-like proprotein processing enzyme of Drosophila melanogaster with multiple repeats of a cysteine motif.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The Dfur2 gene of Drosophila melanogaster: genetic organization, expression during embryogenesis, and pro-protein processing activity off its translational product Dfurin2."; DNA Cell Biol. 14:223-234(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=ISO-1;
MEDLINE=95186060; PubMed=7880443;
Roebroek A.J.M., Ayoubi T.A.Y., Creemers J.W.M., Pauli I.G.L.,
van de Ven W.J.M.;
                                                                                                                                                         Eukaryota; Metazoā; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                 01-APR-1993 (Rel. 25, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Furin-11ke procease 2 precursor (EC 3.4.21.75) (Furin 2)
FUR2 OR CG18724/CG4235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 267:17208-17215(1992).
                                                                                                                                   Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Berkeley;
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Gaps

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2; Indels

1; Mismatches

d

Matches

PRT; 1679 AA.

STANDARD;

RESULT 14
FUR2\_DROME
ID FUR2\_DROME

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FUNCTION: Furin is likely to represent the ubiquitous endoprotease
               activity within constitutive secretory pathways and capable of cleavage at the RX(K/R)R consensus motif (By similarity).
CATALYTIC ACTIVITY: Release of mature proteins from their proproteins by cleavage of Arg-Xaa-Arg-|-Zaa bonds, where Xaa can be any amino acid and Yaa is Arg or Lys. Releases albumin, complement component C3 and von Willebrand factor from their
                                                                                                                                                                                               Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R FLYBase; SG0-10459; Furz.

R GO; GO:0004276; F:furin activity; IDA.

GO:0004276; F:furin activity; IDA.

GO:0004276; F:furin activity; IDA.

R InterPro; IPR0002019; Purin repeat.

InterPro; IPR002084; Peptidase_SB.

InterPro; IPR002084; Peptidase_SBB.

R InterPro; IPR002020; Professe_Inhib.

R Ffam; PF00483; Peptidase_SB; 1.

R PRINTS; PR00717; P-domain; 1.

R PRODOM; PD000717; P-domain; 1.

R PROSITE; PS00134; SUBTILASE_ASP; 1.

R PROSITE; PS00138; SUBTILASE_ASP; 1.

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                                                                                                                                                 respective precursors. Transient expression in a subset of central TISSUE SPECIFICITY: Transient expression in a subset of central nervous avetem neurons during embryonic stages 12-13. Expression in developing tracheal tree from stage 13 to end of embryonic
                                                                                                                                                                                                                                                       DEVELOPMENTAL STAGE: Expressed both maternally and zygotically. SIMILARITY: Belongs to peptidase family S8. Furin subfamily.
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EMBL; L33831; AAA69860.1; -.
EMBL; AE003502; AAF48598.1; -.
PIR; A43434; A43434.
HSSP; Q99405; IMPT.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and physiological diversity.",
Genome Res. 12:532-542(2002).
-!- FUNCTION: Part of a complex that catalyzes the formation of
methyl-coenzyme M and tetrahydromethanopterin from coenzyme M and
methyl-tetrahydromethanopterin. This is an energy-conserving,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATHWAY: Methanogenesis from carbon dioxide; sixth step.
SUBUNIT: The complex is composed of 8 subunits; mtra, mtrs, mtrc, mtrc, mtrc, mtrc and mtrH (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein (Potential).
SIMILARITY: Belongs to the mtrC family.
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                                                                                                                                                                                                                                                                                                                                                                                                         15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Tetrahydromethanopterin S-methyltransferase subunit C (EC 2.1.1.86)
(N5-methyltetrahydromethanopterin-coenzyme M methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sodium-ion translocating step (By similarity)
-!- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin +
mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-
                (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                ..
 (POTENTIAL)
                                                                                                                                                           Length 1679;
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Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
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              (GLCNAC. . . . (GLCNAC. . . . (GLCNAC. . . .
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Pred. No. 1.7e+02;
                                                                  MISSING (IN REF. 1)
V -> F (IN REF. 1)
V -> VDQL (IN REF.
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N-LINKED
N-LINKED
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MEDLINE=21929760; PubMed=11932238;
                                                                                                                         183369 MW;
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15-MAR-2004 (Rel. 43, Last seq.
15-MAR-2004 (Rel. 43, Last anno
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| HAWAP; MF 01096; -; 1. | InterPro; | IPR005865; THM | met_transC. | Prostoin | Mtth | Mtth | Mtth | Mthron | Protation | Mthronogenesis; One-carbon metabolism; Transferase; Methyltransferase; Transmembrane; Complete proteome. | Transmembrane; Complete proteome. | TRANSMEM | 19 | POTENTIAL. | TRANSMEM | 75 | 95 | POTENTIAL. | TRANSMEM | 141 | 151 | POTENTIAL. | TRANSMEM | 162 | 182 | POTENTIAL. | TRANSMEM | 162 | 182 | POTENTIAL. | TRANSMEM | 162 | 182 | POTENTIAL. | TRANSMEM | 162 | 182 | POTENTIAL. | TRANSMEM | 162 | 182 | POTENTIAL. | TRANSMEM | 163 | 184 | POTENTIAL. | TRANSMEM | 164 | 184 | POTENTIAL. | TRANSMEM | 164 | 184 | POTENTIAL. | TRANSMEM | 164 | 184 | POTENTIAL. | TRANSMEM | 164 | 184 | POTENTIAL. | TRANSMEM | 164 | 184 | POTENTIAL. | TRANSMEM | 165 | 184 | POTENTIAL. | TRANSMEM | 164 | 184 | TRANSMEM | 165 | 184 | POTENTIAL. | TRANSMEM | 165 | 184 | POTENTIAL. | TRANSMEM | 165 | 184 | POTENTIAL. | TRANSMEM | 165 | 185 | MW; | POTENTIAL. | TRANSMEM | 165 | MW; | POTENTIAL. | TRANSMEM | 165 | MW; | POTENTIAL. | TRANSMEM | 165 | MW; | POTENTIAL. | TRANSMEM | 165 | MW; | POTENTIAL. | TRANSMEM | 165 | MW; | POTENTIAL. | TRANSMEM | 165 | MW; | POTENTIAL. | TRANSMEM | 165 | MW; | POTENTIAL. | TRANSMEM | 165 | MW; | POTENTIAL. | TRANSMEM | 165 | MW; | POTENTIAL. | TRANSMEM | 165 | MW; | POTENTIAL. | TRANSMEM | 165 | MW; | POTENTIAL. | TRANSMEM | 165 | MW; | POTENTIAL. | TRANSMEM | 165 | MW; | POTENTIAL. | TRANSMEM | 165 | MW; | POTENTIAL. | TRANSMEM | 165 | MW; | POTENTIAL. | TRANSMEM | 165 | MW; | POTENTIAL. | TRANSMEM | 165 | MW; | POTENTIAL. | TRANSMEM | 165 | MW; | POTENTIAL. | TRANSMEM | 165 | MW; | POTENTIAL. | TRANSMEM | MW; | POTENTIAL. | TRANSMEM | POTENTIAL. | TRANSMEM | POTENTIAL. | TRANSMEM | POTENTIAL. | TRANSMEM | POTENTIAL. | TRANSMEM | POTENTIAL. | TRANSMEM | POTENTIAL. | TRANSMEM | POTENTIAL. | TRANSMEM | POTENTIAL. | TRANSMEM | POTENTIAL. | TRANSMEM | POTENTIAL. | TRANSMEM | POTENTIAL. | TRANSMEM | POTENTIAL. | TRANSMEM | POTENTIAL. | TRANSMEM | POTENTIAL. | TRANSMEM | POTENTIAL. | TR
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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93.5%; Score 58; DB 11; Length 1222; 83.3%; Pred. No. 1.1; ive 2; Mismatches 0; Indels (
InterPro; IPR000885; Fib_collagen_C.
Pfam; PF01410; COLFI; 1.
Pfam; PF01391; COLFI; 1.
ProDom; PD000007; Clg helix; 1.
ProDom; PD000007; Clg helix; 1.
ProDom; PD000007; Clg helix; 1.
ProDom; PD000008; COLFI; 1.
Hypothetical protein; Collagen.
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SEQÜENCE 1222 AA; 115140 MW; A409CA00D82765E4 CRC64;
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The RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

"Analysis of the mouse transcriptome based on functional annotation of

"O, 770 full-length cDNAs.";

IN Mature 420:563-573(2002).

IN Mature 420:563-573(2002).

IN MAIL, AKO79113; BAS27545.1; -.

ROS, GO:0005581; C:collagen; IEA.

GO; GO:0005581; C:collagen; IEA.

GO; GO:0005581; C:collagen. C.

InterPro; IPR008160; Collagen. C.

InterPro; IPR008181; Pibrinogen. C.

InterPro; IPR00885; Fib.collagen. C.

PR Pfam; PF01410; COLFI; 1.

PR Pfam; PF01410; COLFI; 1.

PR Pfam; PF01410; Collagen; 1.

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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 338 AA; 35813 MW; 15BE369D8690F37A CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=22354683; PubMed=12466851;
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STRAIN=C57BL/6J; TISSUE=Head;

XX MEDIINE=25354683; PubMed=12466851;

XX The FANTOM Consortium,

A The FANTOM Consortium,

A The FANTOM Consortium,

A The RIKEN Genome Exploration Research Group Phase I & II Team;

Analysis of the mouse transcriptome based on functional annotation of

GO, 700 full-length CDNAs.";

A Malysis of the mouse transcriptome based on functional annotation of

MOS TO TO Full-length CDNAs.";

B MBL; AK046546; BAC33370.1; -.

R MOD; MOI SH845; Col331.

R MOD; MOI SH845; Col331.

R MOD; MOI SH8015; Cold1agen; IEA.

GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

InterPro; IPR00110; Collagen.

InterPro; IPR00110; Collagen.

InterPro; IPR001007; VWF.C.

R InterPro; IPR001107; VWF.C.

R Ffam; PF01410; COLET; 1.B.

PERM; PF01410; COLET; 1.B.

PERM; PF01410; COLET; 1.B.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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ProDom, PD00007; CIg_helix; 1.
SMART; SM00218; COLFI; 1.
SMART; SM00214; VWC; 1.
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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PRT; 1464 AA
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TubercuList; Rv2447c; -.
GO; GO:0005524; F:ATP binding; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; F70863; F70863.
HSSP; P15925; 1FGS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                         Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=H37Rv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     053174;
01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                053174
                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          053174
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                                                                                                                                                                                                                                                                                                                                                       Analysis of Citil Length CDNAs.";

Mature 420:563-573 (2002).

R MGD; MG1184453; CO13a1.

R GO; GO:0005581; C:collagen; IEA.

R GO; GO:0005581; C:collagen; IEA.

GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

R InterPro; IPR008160; Collagen.

R InterPro; IPR008181; Fibrinogen.C.

R InterPro; IPR008181; Fibrinogen.C.

R InterPro; IPR001807; VWF.C.

R InterPro; IPR001807; UWF.C.

R InterPro; IPR001807; UMF.C.

R InterPro; IPR001807; UMF.C.

R InterPro; IPR001807; UMF.C.

R InterPro; IPR001807; UMF.C.

R R InterPro; IPR001807; UMF.C.

R R ProDom; PD00007; C19_helix; 1.

R ProDom; PD00007; C19_helix; 1.

R SMART; SM00018; Fib.collagen.C; 1.
                                                                                                                                                                                                                                                                                            The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CS7BL/6; TISSUE=Brain;

MEDLINE=22388257; PubMed=12477932;

Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 58; DB 11; Length 1464;
Pred. No. 1.3;
2; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1464 AA.
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Aorta, and Vein;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE, PS01208; VWFC 1; 1.
PROSITE; PS50184; VWFC 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.5%;
01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||:||||:|||
1203 IAGVGGEKSGGF 1214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IAGIGGEKAGGF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                    Collagen alpha 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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Matches
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  SO DER REPORT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY 
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Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Sch. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J., Marra M.A., "Generation and intital analysis of more than 15,000 full-length human and mouse cDNA sequences."
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STRANTS-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Eisen J.A., Kaft D., Hickey E.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98295987; PubMed=9634230; Garnier T., Churcher C., Harris D., Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.B. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Kroph A., McLean J., Moule S., Murphy L., Oliver S., Soborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitchead S., Barrell B.G., Bullon J.E., Taylor K., Whitchead S., Barrell B.G., Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.1%; Score 54; DB 11; Length 1464; 75.0%; Pred. No. 5.9; ive 2; Mismatches 1; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. EMBL, BC052398, AAH52398.1; -. Hypothetical protein. SEQUENCE 1464 AA; 138971 MW; 2B38BC27AF21590B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO21246; CAA16024.1; -.
EMBL; AE007089; AAK46822.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Polylpolyglutamate synthase.
FOLC OR RV2447C OR MIV008.03C OR MT2523.
                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 06, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 75.0%;
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | |:||||:|||
1203 IVGVGGEKSGGF 1214
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Pu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Shao Y., Yin H.F., Zhang Y., Cal Z., Chen J., Kang H., Chen X.Y., Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu Y.R.H., Li C., Li T., Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Hong G.F.; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21608551; PubMed=11743194; Godner B., Hinkle G., Gattung S., Miller N., Blanchard M., Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L., Qurollo B., Goldman B.S., Cao Y., Akenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Gielo C., Slater S., Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                   MEDLINE=2160856; PubMed=11743193; Mood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland B., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D. Shang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (Rice).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poacese;
Ehrhartoidese, Oryzae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.7%; Score 42; DB 16; Length 209; 72.7%; Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21865 MW; B09845588049D0C6 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
OSJNBA0011K22.12 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1755 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; AE2981; AE2981.

PIR; C98102; C98302.

G0:00003824; F:catalytic activity; IEA.
InterPro; IPR001087; Lipase_GDSL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE009275; AAL44267.1; -. EMBL; AE008336; AAK89941.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00657; Lipase GDSL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 VAGPGGEPAGG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IAGIGGEKAGG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0004326; F:tetrahydrofolyplolyglutamate synthase activity; IEA.
GO; GO:00049058; P:biosynthesis; IEA.
GO; GO:0009396; P:biosynthesis; IEA.
GO; GO:000396; P:folic acid and derivative biosynthesis; IEA.
InterPro; IPR001645; Ppolygl synthtse.
InterPro; IPR0011; Mur_ligase_C.
InterPro; IPR004101; Mur_ligase_C.
Pfam; PF01225; Mur_ligase_1.
Pfam; PF01255; Mur_ligase_1.
IIGRFAMS; IIGR01499; folc.
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable folylpolyglutamate synthase protein FOLC
(Folylpoly-gamma-glutamate synthetase) (FPGS) (EC 6.3.2.17).
FOLC OR MB2474C.
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ADA OR ATU3454 OR AGR L 2749.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Rhizobium/Agrobacterium group; Agrobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 16; Length 487;
Pred. No. 78;
0; Mismatches 1; Indels
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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90.0%;
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Best Local Similarity
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Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probable aminomethyltransferase (Glycine cleavage system T protein) (EC 2.1.2.10).
GCVT OR R01549 OR SMC02047.
                                                                                                                                                                                                        01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
00-0051A11.6 protein (0J116 C07.6 protein).
00-0051A11.6 OR 0J116 C07.6 protein).
00-0052 sativa (japonica cultivar-group).
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Sasakī T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
clone:0J1116_C07";
                                                                                                                                                                                                                                                                                                                                                     SEGUENCE FROM N.A. STRAINECY. Matsunoto T., Yamamoto K.; Sasaki T., Matsunoto T., Yamamoto K.; Cryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                   Query Match 67.7%; Score 42; DB 10; Length 1755; Best Local Similarity 66.7%; Pred. No. 6.2e+02; Matches 8; Conservative 1; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.1%; Score 41; DB 10; Length 208; 54.5%; Pred. No. 98; 2; Indels iive 3; Mismatches 2; Indels
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Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
EMBL; AL731644; CAE05230.1; -.
SEQUENCE 1755 AA; 198541 MW; 9BCC452826914DB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          clone:P0551A11.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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EMBL, AP004253; BAC00689.1; -.
GZTAMEDE, Q81418; -.
SEQUENCE 208 AA; 20670 NW; C4D641DBA4D55B80 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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232 IAGESGDKGGGF 243
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                                                                                         1 IAGIGGEKAGGF 12
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63 VGGVGGREAGG 73
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Q92Q09
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Q8L418
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E. EMBL, AL591787; CAC46128.1; -
E. CO GO:00040477; F:aminomethyltransferase activity; IEA.

GO; GO:0004374; F:glycine cleavage system; IEA.

R GO; GO:0016546; P:glycine catabolism; IEA.

R GO; GO:0016546; P:glycine catabolism; IEA.

R HIACEPRO; IPRO06223; GCV T.
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Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankala, A.,
Kosugi H.,
Hosoyama A., Pukui S., Nagazi Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-II., Kubota K.,
"Complete genome sequence of an aerobic hyper-thermophilic
cranarchaeon, Aeropyrum pernix Kl.";
EMBL, AP000058; BAA79121.1; -.
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Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
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GO; GO:0004222; F:metalloendopeptidase activity; IEA.
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0007422; P:intracellular signaling cascade; IEA.
GO; GO:000508; P:intracellular signaling cascade; IEA.
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PROSITE; PS0142; ZINC_PROTEASE; 1.
SEQUENCE 383 AA, 39729 MW; FE7289C4F06E8F76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transferase; Complete proteome.
SEQUENCE 379 AA; 40369 MW; 047C7002EF5A30CF CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
383AA long hypothetical S2P metalloprotease.
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InterPro; IPR008915; Peptidase_M50.
InterPro; IPR001915; Pept M50_SREBP.
InterPro; IPR006025; Pept_M_Zn_BS.
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MEDLINE=99310339; PubMed=10382966;
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SMART; SM00228; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Desulfurococcaceae; Aeropyrum.
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TIGRFAMB; TIGR00528; gcvT; 1.
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Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tauch A.,

Tauch A.,

"The IncP beta plasmid pB4 encodes a tripartite antibiotic efflux system of the RND-MEP-OEP type conferring erythromycin and roxithromycin resistance in Pseudomonas sp. B13.";

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ431260; CAD24375.1; -.

EMBL; AJ431260; CAD24375.1; -.

GO; GO:0009291; P:unidirectional conjugation; IEA.

InterPro; IPR005498; TrbI.

Fiam; PF03743; TrbI; 1.
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Gruidl M.E., Smith P.A., Kuznicki K.A., McCrone J.S., Kirchner J.,
Strome S., Bennett K.L.;
Strome G., Bennett K.L.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
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Score 41, DB 17; Length 383;
Pred. No. 1.9e+02;
0; Mismatches 2; Indels
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GO; GO:0008026; F.ATP dependent helicase activity; IEA.
GO; GO:0016787; F.hydrolase activity; IEA.
GO; GO:0003676; F.nucleic acid binding; IEA.
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Last annotation update)
                                                                                                                                                                                                                                                                                                       460 AA.
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NCBI_TaxID=77133;
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Plasmid pB4.
  66.1%;
80.0%;
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EMBL; U60194; AAB0337.1; -.
HSSP; Q58083; 1HV8.
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
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                                                      8; Conservative
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211 SGVGGQQAGG 220
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                                      InterPro; IRRO0619; DEAD box.
InterPro; IPR001659; Helicase C.
InterPro; IPR001650; Helicase C.
InterPro; IPR001650; Helicase C.
InterPro; IPR00184; Znf CCHC.
Pfam; PF00271; helicase C; 1.
Pfam; PF00271; helicase C; 1.
Pfam; PF00299; Z-CCHC; 6.
PRINTS; PR00999; Z-CCHC; 6.
SWART; SW00449; DEAD ILC; 1.
SWART; SW00490; HELICC; 1.
SWART; SW0039; DEAD ATP_HELICASE; 1.
PROSITE; PS00039; DEAD ATP_HELICASE; 1.
PROSITE; PS00189; Znf CCHC; 6.
ROSITE; PS00189; PF CCHC; 6.
ROSITE; PS0186; ZP CCHC; 6.
RATP-binding; Helicase; Hydrolase.
SEQUENCE 974 AA; 100426 MW; BF994CA586D86C71 CRC64;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 18, 2004, 03:47:39 Run on:

99; Search time 26.7647 Seconds (without alignments) 52.784 Million cell updates/sec

US-10-615-959-44 26 1 EKAGG 5 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:\* geneseqp2000s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* A Geneseq 29Jan04:\* ٠. Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Aari2514 Part of the Aab61739 Human typ Aar71720 Potential Aab6119 Collagen Aab61721 Human colladen Aab61722 Human colladen Aab61722 Human typ Aab61722 Human typ Aab61724 Human typ Aab61725 Human typ Aab61725 Human typ Aab61726 Human typ Aab61726 Human typ Aab61726 Human typ Aab61726 Human typ Aab61726 Human typ Aab61726 Human typ Aab61721 Human typ Aab61721 Human typ Aab61721 Human typ Aab61721 Human typ Aab61721 Human typ Aab61721 Human typ Aab61721 Human typ Aab61721 Human typ Aab61721 Human typ Aab61721 Human typ Aab61721 Human typ Aab61729 Human typ Aab61729 Human typ Aab61729 Human typ Aab61729 Human typ Aab61729 Human typ Aab61729 Human typ Aab61729 Human typ Aab61729 Human typ Aab61729 Human typ Aab61729 Human typ
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Abb56496 Human MHC Aae38626 Human N-t Aam98908 Vaccine r Abr43102 Human T-c Aae37759 TIRC7 pep Aae37809 TIRC7 pep Aae37809 TIRC7 pep Aae37809 TIRC7 pep Aar92068 Recombina Aar92068 Recombina Aar92068 Recombina Abp33968 Human ORF Aag15968 Arabidops Amm13314 Peptide # Abb38630 Peptide # Abb38630 Peptide # Abb23630 Peptide # Abb23723 Protein # Abb23723 Protein # Abm22723 Human bon	Human	
ABB56496 AAE38626 AAM98908 AAM98908 AAE31759 AAE31769 AAR92068 AAR92068 AAR92068 AAR15314 AAM11803 AAM11802 AAM71809	ABG53486 ABG41615	AAB24662
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## ALIGNMENTS

RESULT 1  AAR12514  XX  XX  XAR12514  XX  AAR12514;  XX  AAR12514;  XX  AAR12514;  XX  AAR12514;  XX  AAR12514;  XX  AAR12514;  XX  AAR12514;  XX  ADT 12-SEP-1991 (first entry)  XX  Bert of type III collagen telopeptide.  XX  Wow os sapiens.  XX  Homo sapiens.  XX  XX  XX  XX  XX  XX  XX  XX  XX
inda: (re (fi inf inf inf inf inf ing 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9

Detection of collagen degradation peptide(s) - used for detecting, diagnosing and monitoring degenerative and inflammatory disorders. WPI; 1991-193334/26.

The peptide is part of a larger molecule to which it is linked via the lysine in the 2 posn: Glu-Hyl-Ala-Gly-Gly-Phe. . . (AAR12514) CC | Glu-Hyl-Ala-Gly-Gly-Phe. . . (AAR12514) CC | Glu-Hyl-Ala-Gly-Gly-Phe CC | Hyl Hyl-Hyl-Hyl = hydroxylysl pyridinion. The peptide, or a similar molecule hadring the pyridinium ring cleaved, can be detected in body fluid using a specific binding partner. The amt. present gives an indication of bone resorption and can be used to screen for osteoarthritis and similar degenera- tive and inlammatory disorders. The peptide was prepd. from human urine using reverse phase and molecular sleve chromatography. See also AAR12510-R12513. (Updated on 25-MAR-2003

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AAR71720 standard; protein; 7 AA.
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EKAGG 5
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              type
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assay for detecting cross-linked telopeptide analytes indicative of II collagen resorption in vivo in a body fluid sample, comprises contacting the sample with an antibody which binds to the analyte.
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                                                                                                                                                                                                                                  Type II collagen, immunoassay, cartilage, telopeptide; human; type III collagen.
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                                         100.0%; Score 26; DB 2; Length 6; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                               Human type III collagen carboxy-telopeptide fragment.
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                                                                                                                                                        AAB61739 standard; peptide; 6 AA.
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99US-0142274P.
99US-0142675P.
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                                                                5; Conservative
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Best Local Similarity
     to correct PA field.)
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                                        Query Match
Best Local Similarity
Matches 5; Conserv
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                           Sequence 6 AA;
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02-JUL-1999;
07-JUL-1999;
30-AUG-1999;
                                                                                                                                                                                                                                                                                                                                      10-DEC-1999;
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Determination of collagen fragments in body fluids can be achieved by communoassay using antibodies directed against synthetic peptides derived from collagen which contain sites of potential crosslinking. The method compared to disorders of collagen which contains itses of potential crosslinking. The method compared to disorders of collagen may indicate osteoporosis, metastatic progression, Paget's disease, hyperthyroidism or other conditions involving excessive bone resorption; degredation of type II collagen may indicate rheumatoid arthritis or osteoarthritis; and of type II collagen, vaculitis syndrome). The method can also be used to assess the toxicity of a compound and to test drugs for their effect on collagen metabolism. The sequences of collagen fragments on which the synthetic peptides were based are described in AAR17705.07 and ARR17709-12. This clopetide sequence is a potential cross-linking site in collagen alphal (type III) and is found at the C-terminus. (Updated on 25-MAR-2003 to
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                                                                                                                                                  Collagen; antibody; immunoassay; metabolism; diagnosis; monitoring; disorder; osteoporosis; metastatic progression; Paget's disease; hyperthyroidism; bone; resorption; rheumatoid arthritis; osteoarthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assaying collagen fragments in body fluid by immunoassay - using antibodies raised against synthetic peptide(s) contg. potential crosslinking sites, to diagnose and monitor disorders of collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
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                                                                                        Potential cross-linking sequence of collagen type III.
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100.0%; Pred. No. 1.4e+06;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  metabolism, e.g. osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94WO-DK000348
(revised)
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                                                                                                                                                                                                                                                                  vasculitis syndrome
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25-MAR-2003
18-OCT-1995
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Conservative

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                                                                                                                                                                                     Collagen type III; vasculitis syndrome; assay; diagnosis.
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                                                                                                                         Collagen type III alpha-1 C-terminal peptide.
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The invention relates to immunoassays for measuring type II collagen (aartilage) resorption in vivo. The method of analysing a body fluid sample for the presence of an analyte indicative of a physiological condition, involves contacting the body fluid sample with an antibody fluid sample, and correlating any detected binding of Ab in the body fluid sample, and correlating any detected binding to the physiological condition. The analysis is useful for measuring type II collagen non-mineralized and mineralized cartilage, and for measuring total cartilage resorption in vivo. The present sequence represents a peptide based on the carboxy-terminal telopeptide sequence of human collagen II, to which an antibody binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; collagen type III; osteoporosis; bone resorption; Paget's disease; hyperparathyroidism; rheumatoid arthritis; osteoarthritis; therapy; vasculitis syndrome; toxic substance; tissue degradation; alphal(III).
                                                                                                                                                                                                                                                        Assay for detecting cross-linked telopeptide analytes indicative of type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                      II collagen resorption in vivo in a body fluid sample, comprises contacting the sample with an antibody which binds to the analyte.
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                                                                                                                                                                                                                                                                                                                  Claim 1; Page 16; 34pp; English.
                                                                      99US-00335098.
99US-0141574P.
99US-0142274P.
99US-0142675P.
                                            99WO-US029357
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97US-00963825.
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Best Local Similarity
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04-NOV-1997;
              28-DEC-2000
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The invention relates to a peptide synthesised to match an alphal(I) or alpha2(I) telopeptide component of a cross-linked telopeptide degradation of product of type I collagen. The method is useful for assaying collagen to fragments in animal body fluids, for determining the degradation of human collagen types I, II and III and for diagnosing the presence of disorders associated with the metabolism of collagen, especially osteoporosis. The peptide is used for assessing the impact of drugs on collagen metabolism. The peptide is useful in methods to assess an abnormal condition of a subject for e.g. excessive bone resorption which shows the presence of an costeoporotic condition or the metastatic progress of a malignancy, agent's disease and hyperparathyroidism. Disease states involving connective tissues can be monitored by determining collagen degradation, examples are collagen type III degradation associated with rheumatoid arthritis, osteoarthritis, and collagen type III degradation in continuously, application of these assays can also be used to monitor the progress of thorapy administered to treat these or other conditions and as a measure of toxicity, since the administration of toxic substances of the insure degradation. The present sequence is human collagen type III alpha1(III) C-terminal peptide used for synthesising a peptide used in the invention
                                                                                 peptides that match alpha 1 or 2(I) telopeptide component of telopeptide degradation product of type I collagen useful sing disorders associated with collagen metabolism e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB80730 standard; peptide; 7 AA.
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Matches 5: Conserv
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04-NOV-1997;
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                                                                                                                       diagnosing
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                Qvist P,
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sapiens. 21-JAN-1994; US6342361-B1 04-NOV-1997; 29-JAN-2002 ABB09622; Ovist P, Ношо ö Collagen; osteoarthritis; Paget's disease; Marfan syndrome; dwarfism; osteogenesis imperfecta; neoplastic growth; rheumatoid arthritis; vasculitis. Gaps ö 100.0%; Score 26; DB 5; Length 7; 100.0%; Pred. No. 1.4e+06; 0; Indels Collagen type III-alphal C-terminal fragment. Mismatches ..

Disclosure; Col 9-10; 35pp; English

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                                                                                                                                                               The invention relates to a method for assaying type I collagen fragments (1) in body fluid. The method involves treating the test sample with: (i) synthetic peptide, immobilised on a support; and (ii) immunological binding partner, reactive with the synthetic peptide, so that (I) and the synthetic peptide compete for binding, and (I) are quantified by measuring the binding of the binding partner to the synthetic peptide. The method is used to diagnose disorders of collagen metabolism. The method is used to diagnose disorders of collagen metabolism, osteogenesis imperfecta, neoplastic growth of collagenous tissue, dwarfism, theumatoid arthritis or vasculitis, also for clinical testing of drugs to assess their effect on collagen metabolism. Sequences ABBB0716-732 represent synthetic peptides derived from collagen used for assaying type I, II and III collagen fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assaying type II collagen fragments in a body fluid sample, for determining abnormalities in collagen metabolism, e.g. in Paget's disease or Marfan's syndrome, comprises contacting the fluid with a synthetic type II collagen alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Collagen; bone resorption; collagen metabolism; Paget's disease;
Marfan's syndrome; osteogenesis imperfecta; neoplastic growth; dwarfism;
rheumatoid arthritis; osteoarthritis; vasculitis syndrome.
                                                             Assaying type I collagen fragments in body fluid, useful for diagnosis and assessing treatment of e.g. osteoarthritis, by competitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                       Disclosure; Col 7-8; 35pp; English.
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97US-00963825.
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                               WPI; 2002-380937/41
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Best Local Similarity
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Qvist P,
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The present sequence represents a peptide derived from collagen type III alphal. The peptide has potential sites for crosslinking to various collagens. The specification describes a method for assaying type II collagen fragments in a body fluid sample. The method comprises contacting the body fluid with a synthetic peptide consisting essentially of a type II collagen alphal maino acid sequence that competes with the collagen fragments for binding with the immunological binding partner. The method is useful for assaying collagen fragments in body fluids. The method is particularly useful in assays for measuring bone resorption rates in patients or in healthy subjects. The method may be used for determining abnormalities in collagen metabolism, especially in Paget's disease, Marfan's syndrome, osteogenesis imperfecta, neoplastic growth in collagenous tissue, dwarfism, rheumatoid arthritis, osteoarthritis or vasculitis syndrome. The method may be used for determining the degradation of human collagen of type I, II and III. It also can be used during clinical testing of new drugs to assess the impact of these drugs on collagen metabolism. The assays, can be used as a measure of toxicity, since the administration of toxic substances often results in tissue metabolis condition. Thus, the assays may be applied in any situation where the condition, treatment or effect of substances druckly administered to the condition, treatment or effect of substances directly administered to the
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100.0%; Score 26; DB 5; Length 7; Larity 100.0%; Pred. No. 1.4e+06; Conservative 0; Mismatches 0; Indels Similarity 5; Conserva Ŋ Sequence 7 AA; Query Match Best Local Best Loca Matches

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RESULT 9 AAB6172

AAB61722 standard; peptide; 8 AA. AAB61722; 

(first entry) 20-APR-2001

Human type II collagen carboxy-telopeptide fragment.

Type II collagen; immunoassay; cartilage; telopeptide; human.

Homo sapiens. Synthetic.

WO200079284-A1.

28-DEC-2000

99US-00335098. 99US-0141574P. 99US-0142274P. 17-JUN-1999; 29-JUN-1999; 02-JUL-1999

99WO-US029357.

10-DEC-1999;

99US-00385740 99US-0142675P 30-AUG-1999; 07-JUL-1999

(WASH-) WASHINGTON RES FOUND

Eyre DR;

WPI; 2001-146859/15.

Assay for detecting cross-linked telopeptide analytes indicative of type II collagen resorption in vivo in a body fluid sample, comprises contacting the sample with an antibody which binds to the analyte.

Disclosure; Page 7; 34pp; English.

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          (cartilage) resorption in vivo. The method of analysing a body fluid sample for the presence of an analyte indicative of a physiological condition, involves contacting the body fluid sample with an antibody (Ab) which binds to the analyte, detecting binding of Ab in the body fluid sample, and correlating any detected binding to the physiological condition. The analysis is useful for measuring type II collagen (cartilage) resorption in vivo, for distinguishing between resorption of non-mineralized and mineralized cartilage, and for measuring total synthetic peptide based on the carboxy-terminal telopeptide sequence of human collagen type II
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The invention relates to immunoassays for measuring type II collagen
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cartilage resorption in vivo. The present sequence represents a linear synthetic peptide based on the carboxy-terminal telopeptide sequence of human collagen type III
                                                                                               Gaps
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100.0%; Pred. No. 1.4e+06;
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02-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assay for detecting cross-linked telopeptide analytes indicative of type II collagen resorption in vivo in a body fluid sample, comprises contacting the sample with an antibody which binds to the analyte.
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; Pred. No. 1.4e+06;
0; Mismatches 0;
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                                                                                                                                                      AAB61725 standard; peptide; 9 AA.
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99US-0141574P.
99US-0142274P.
99US-0142675P.
99US-00385740.
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WO200079284-A1

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The invention relates to immunoassays for measuring type II collagen (cartilage) resorption in vivo. The method of analysing a body fluid sample for the presence of an analyte indicative of a physiological condition, involves contacting the body fluid sample with an antibody fluid sample, and correlating any detected binding of Ab in the body fluid sample, and correlating any detected binding to the physiological condition. The analysis is useful for measuring type II collagen (cartilage) resorption in vivo, for distinguishing between resorption of non-mineralized and mineralized cartilage, and for measuring total cartilage resorption in vivo. The present sequence represents a linear synthetic peptide based on the carboxy-terminal telopeptide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                               Assay for detecting cross-linked telopeptide analytes indicative of type II collagen resorption in vivo in a body fluid sample, comprises contacting the sample with an antibody which binds to the analyte.
                                                                           Type II collagen; immunoassay; cartilage; telopeptide; human.
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                                              Human type II collagen carboxy-telopeptide fragment.
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99US-0141574P.
99US-0142274P.
99US-0142675P.
99US-00385740.
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               20-APR-2001 (first entry)
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AAB61741
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The invention relates to immunoassays for measuring type II collagen (cartilage) resorption in vivo. The method of analysing a body fluid sample for the presence of an analyte indicative of a physiological condition, involves contacting the body fluid sample which hinds to the analyte, detecting binding of Ab in the body fluid sample, and correlating any detected binding to the physiological condition. The analysis is useful for measuring type II collagen (cartilage) resorption in vivo, for distinguishing between resorption of non-mineralized and mineralized cartilage, and for measuring total cartilage resorption in vivo. The present sequence represents a linear synthetic peptide based on the carboxy-terminal telopeptide sequence of
                                                                                                                                                                                                                                                                   Assay for detecting cross-linked telopeptide analytes indicative of type II collagen resorption in vivo in a body fluid sample, comprises contacting the sample with an antibody which binds to the analyte.
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100.0%; Pred. No. 1.4e+06;
rative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB61726 standard; peptide; 10 AA.
                                                                                                            99US-0141574P.
99US-0142274P.
99US-0142675P.
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99US-0141574P.
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Matches 5; Conservative
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29-JUN-1999;
02-JUL-1999;
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Gaps ö

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 Query Match
 100.0%; Score 26; DB 4; Length 10;

 Best Local Similarity
 100.0%; Pred. No. 43;

 Matches
 5; Conservative
 0; Mismatches
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 1 EKAGG 5

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 3 EKAGG 7

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Search completed: September 18, 2004, 04:25:35 Job time : 28.7647 secs

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September 18, 2004, 04:20:54; Search time 8.23529 Seconds (without alignments) 31.344 Million cell updates/sec
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2: /cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/jaa/PCTUS COMB.pep:*
6: /cgn2_6/ptodata/2/jaa/PCTUS COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum DB seq length: 2000000000
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Result No.	Score	Query	Query Match Length	DB	ID	Description	
П	26	100.0	ß	4	US-10-009-999A-44	Segmence 44	Appl
N	26	100.0	9	4	US-10-009-999A-39	' m	Appl
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4	56	100.0	7	m	-397B-	Segmence 16.	Appl
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ø	26	100.0	7	4	US-09-570-573-15	-	Appl
7	56	100.0	7	4	US-09-385-740B-21	N	Appl
ω	26	100.0	7	4	US-09-548-608-15	Sequence 15.	Appl
σ	56	100.0	7	4	US-09-714-146-16	Н	Appl
07	26	100.0	7	4	9	7	Appl
77	26	100.0	7	4	US-10-009-999A-21	6	Appl
12	56	100.0	80	4	US-09-385-740B-22	2	Appl
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14	26	100.0	80	4	-10-073-	~	Appl
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16	26	100.0	8	4	US-10-009-999A-22	N	Appl
17	26	100.0	89	4	-10-	N	Appl
18	26	100.0	80	4	US-10-009-999A-40	4	Appl
13	26	100.0	σ	4	US-09-385-740B-23	N	Appl
20	26	100.0	σ	4	US-09-385-740B-25		App1
21	56	100.0	σ	4	US-10-073-679-23	N	Appl
22	56	100.0	σ'n	4	US-10-073-679-25	~	Appl
23	56	100.0	σ	4	US-10-009-999A-23	2	Appl
24	56	100.0	σ	4	US-10-009-999A-25	2	Appl
25	26	100.0	σ	4	US-10-009-999A-41	4	Appl
56	26	100.0	10	4	9	2	Appl
27	56	100.0	10	4	N	10	רמת

Gaps

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Query Match

Query Match

100.0%; Score 26; DB 4; Length 5;

Best Local Similarity 100.0%; Pred. No. 3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels

1 EKAGG 5 ||||| 1 EKAGG 5

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Sequence 39, Application US/10009999A
; Patent No. 6602980
; GENERAL INFORMATION:
APPLICANT: Eyre, David R.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS

US-10-009-999A-39

RESULT 2

NAME/KEY: MISC FEATURE

OTHER INFORMATION: synthetic peptide corresponding to carboxy-terminal

CHER INFORMATION: telopeptide sequence of human type III collagen

US-10-009-999A-44

Sequence 26, Appl Sequence 31, Appl Sequence 31, Appl Sequence 42, Appl Sequence 30, Appl Sequence 30, Appl Sequence 43, Appl Sequence 27, Appl Sequence 27, Appl Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 29,	COLLAGEN RESORPTION ASSAYS	
US-10-009-999A-26 US-31 US-10-009-999A-31 US-10-009-999A-31 US-10-009-999A-42 US-10-009-999A-42 US-10-009-999A-42 US-10-009-999A-43 US-10-009-999A-43 US-10-009-999A-43 US-10-009-999A-43 US-10-009-999A-43 US-10-009-999A-27 US-10-009-999A-28 US-10-009-999A-28 US-10-0073-679-28 US-10-0073-679-28 US-10-0073-679-28 US-10-0073-679-28 US-10-0073-679-28 US-10-0073-679-28 US-10-0073-679-29	GNMENTK ES FOR 9,999A 9357 098 574	60/142 09/385 2
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Sequence 16, Application US/08817397B Patent No. 6210902
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                15:
                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                         H: 7 amino acids
amino acid
OGY: linear
               TELEX: 236687
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
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212-753-6237
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppadish

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/187,319

FILING DATA:

APPLICATION NUMBER: US/08/187,319

FILING DATA:

ATTORNEY/AGENT INFORMATION:

NAME: GOGORIS, Adda C
FILE REFERENCE: WROS-1-18220
CURRENT APPLICATION NUMBER: US/10/009,999A
CURRENT PILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: PCT/US99/29357
PRIOR PILING DATE: 1999-12-10
PRIOR PILING DATE: 1999-10-17
PRIOR PILING DATE: 1999-06-17
PRIOR PILING DATE: 1999-06-27
PRIOR PILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: US 60/142,574
PRIOR APPLICATION NUMBER: US 60/142,675
PRIOR APPLICATION NUMBER: US 60/142,675
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/142,675
PRIOR APPLICATION NUMBER: US 60/142,675
PRIOR APPLICATION NUMBER: US 09/385,740
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 09/385,740
PRIOR APPLICATION NUMBER: US 09/385,740
PRIOR SEQ ID NOS: 45
SOFTWARE: PACENTIN VETSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REPERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION:
TELEPHONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 3
US-08-963-825-15
US-08-963-825-15
; Sequence 15, Application US/08963825
; Patent No. 6110689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: GVISE, PER APPLICANT: Bonde, Martin TITLE OF INVENTION: A Method TITLE OF INVENTION: Method TITLE OF INVENTION: Disorded TITLE OF SEQUENCES: 21 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 39
LENGTH: 6
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ESTIMATION OF THE FRAGMENTATION PATTERN OF COLLAGEN IN BODY FLUIDS AND THE DIAGNOSIS OF DISORDERS...
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                                                                                                                             100.0%; Score 26; DB 3; Length 7; 100.0%; Pred. No. 3e+05;
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN TYPE III - ALPHA 1 - C TERM
US-08-963-825-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTAIN USA CONTINUE IN USA CONTINUE IN USA COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: IBM COMPATA: APPLICATION NUMBER: US/08/817,397B FILING DATE: 1-UW-1997 CLASSIFICATION DATA: APPLICATION NUMBER: PCT/RE95/04055 FILING DATE: 11-OCT-1995 APPLICATION NUMBER: DK 1194/94 FILING DATE: 17-OCT-1995 APPLICATION NUMBER: DK 1194/94 FILING DATE: 17-OCT-1995 APPLICATION NUMBER: DK 1194/94 FILING DATE: 17-OCT-1995 APPLICATION NUMBER: 25.736 ATTORNEY/AGENT INFORMATION: NAME: Lawrence, III, Stanton T NAME: Lawrence, III, Stanton T NAME: Lawrence, III, Stanton T NAMES CONTAINS OF THE OWN NUMBER: 25.736 REFERENCE/DOCKET NUMBER: 25.736 REFERENCE/DOCKET NUMBER: 25.736
                                                                                                                                                                                     0; Mismatches
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APPLICANT: QVIST, Per
APPLICANT: QVIST, Per
TITLE OF INVENTION: BSTIMATION OF THE
TITLE OF INVENTION: PSTIMATION OF THE
TITLE OF INVENTION: PSTIMATION OF CLIAGEN
TITLE OF INVENTION: OF DISORDERS...
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
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Sequence 15, Application US/09570573

Patent No. 6342361

GENERAL INFORMATION:

APPLICANT: Ovist, Per
APPLICANT: Bonde, Martin

TITLE OF INVENTION: A Method for Assaying Collagen Fragments

TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of TITLE OF INVENTION: Disorders Associated with the Metabolism of TITLE OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC

STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 7;
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                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/570,573
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Fatent No. 6348320
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REPERENCE: WROS.1-14269
CURRENT FILING DATE: 1999-08-30
FRICR PILING DATE: 1999-08-30
PRIOR APPLICATION NUMBER: US 60/142,274
PRIOR APPLICATION NUMBER: US 60/142,274
PRIOR APPLICATION NUMBER: US 60/142,274
PRIOR APPLICATION NUMBER: US 60/142,274
PRIOR APPLICATION NUMBER: US 60/142,274
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CLONE: COLLAGEN TYPE III - ALPHA 1 - C TERM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gegoris, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEFHONE: 212-527-7700
TELEFAX: 212-753-6237
                                                                                                                                                                                                                     STREET: BOS Third Avenue CITY: New York COUNTRY: USA ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
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FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
COMPUTER: IBM FC COMPO
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                 APPLICANT: Orist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Method for Assaying Collagen Fragments
TITLE OF INVENTION: In Body Fluids, A Test Kit and Means for Carrying Out the
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
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                                           100.0%; Score 26; DB 3; Length 7; 100.0%; Pred. No. 3e+05;
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                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
GOTTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/09/500,811
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OKGANISM:
IMMEDIATE SOURCE:
CLONE: COLLAGEN TYPE III - ALPHA 1 - C TERM
                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REPERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
                                                                                                                                                                                                                                                      US-09-500-811-15
; Sequence 15, Application US/09500811
Patent No. 6323314
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 23687
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
                                       Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Matches 5; Conserv
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                                                                                                                             1 EKAGG 5
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US-08-817-397B-16
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RESULT

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GENERAL INFORMATION:
APPLICANT: Per Qvist
APPLICANT: Martin Bonde
ITILE OF INVENTION: A Method of Characterizing the Degradation of Type II Collagen
ITILE OF INVENTION: A Method of Characterizing the Degradation of Type II Collagen
FILE REFERENCE: 8969-020-999
CURRENT APPLICATION NUMBER: US/09/714,146
CURRENT FILING DATE: 1997-06-11
PRIOR APPLICATION NUMBER: 08/817,397
PRIOR APPLICATION NUMBER: 956650
PRIOR FILING DATE: 1995-10-16
PRIOR FILING DATE: 1995-10-16
PRIOR FILING DATE: 1995-0-11
PRIOR FILING DATE: 1994-10-17
PRIOR FILING DATE: 1994-10-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 20
SECTION 16
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                                                                                                             Score 26; DB 4; Length 7; Pred. No. 3e+05;
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Patent No. 6566492

GENERAL INFORMATION:

APPLICANT: EYE, David

TITLE OF INVENTION: CARTILAGE RESORPTION ASSAYS

FILE REFERENCE: WROS.1-142671

CURRENT APPLICATION NUMBER: US/10/073,679

CURRENT FILING DATE: 2002-02-11

PRIOR FILING DATE: 1999-06-30

PRIOR FILING DATE: 1999-06-20

PRIOR FILING DATE: 1999-06-20

PRIOR FILING DATE: 1999-06-20

PRIOR PLING DATE: 1999-06-20

PRIOR PLING DATE: 1999-06-17

PRIOR PLING DATE: 1999-06-17

PRIOR FILING DATE: 1999-06-17

PRIOR FILING DATE: 1999-06-17

PRIOR FILING DATE: 1999-06-17

PRIOR FILING DATE: 1999-06-17

PRIOR FILING DATE: 1999-06-17

SOFTWARE: Patentin Version 3.0

SEQ ID NO 21
                     i IMMEDIATE SOURCE:
; CLONE: COLLAGEN TYPE III - ALPHA 1 - C TERM
US-09-548-608-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 3e+
Matches 5; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                     US-09-714-146-16
; Sequence 16, Application US/09714146
; Patent No. 6372442
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Best Local Similarity 100.
Matches 5; Conservative
    Homo sapiens
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US-09-714-146-16
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TYPE: PRT
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                                                                                                                                                                                                                                                                          NAME/KEY: PEPTIDE : LOCATION: (1)..(7) : OTHER INFORMATION: syn-corr. to N-terminal telopeptide seq. of hu. type II collagen US-09-385-740B-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Ovist, Per
APPLICANT: Ovist, Per
APPLICANT: Ovist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the
TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
TITLE OF INVENTION: Disorders Associated with the Metabolism of
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/548,608

FILING DATE:

ATHORNEY/AGENT INFORMATION:

NAME: GOGOTIS, Add C REGISTATION NUMBER: 29,714

REFERENCE/DOCKET NUMBER: 29,714

REFERENCE/DOCKET NUMBER: 29,714

TELEPPAX: 212-753-6237

TELEPPAX: 212-753-6237
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/335,098
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-19
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.0
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/09548608 Patent No. 6355442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
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FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 212-753-6237
TELEX: 23687
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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3Y: linear
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2 EKAGG 6
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US-09-548-608-15
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NAME/KEY: PEPTIDE LOCATION: (1)..(8) OTHER INFORMATION: syn- corr. to N-terminal telopeptide seq. of hu. type II collagen
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; OTHER INFORMATION: syn- corr. to N-terminal telopeptide seq. of hu. type II collagen
US-09-385-740B-24
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100.0%; Score 26; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels
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Patent No. 6348320
GENERAL INFORMATION:
APPLICANT: Eyre, David
TITLE OF INVENTION: CARTILAGE RESORPTION ASSAYS
FILE REFERENCE: WROS-1-14269
CURRENT APPLICATION NUMBER: US/09/385,740B
CURRENT FILING DATE: 1999-08-30
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Patent No. 6566492
GENERAL INFORMATION:
APPLICANT: Eyre, David
TITLE OF INVENTION: CARTILAGE RESORPTION ASSAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                 PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/335,098
PRIOR APPLICATION NUMBER: US 60/089,823
PRIOR APPLICATION NUMBER: US 60/089,823
PRIOR FILING DATE: 1998-06-19
NUMBER OF SEQ ID NOS: 31.
SEGTWARE: Patentin version 3.0
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/142,274
PRIOR FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: US 60/141,574
PRIOR APPLICATION NUMBER: US 09/335,098
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1998-06-19
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.0
LENGTH: 8
PRIOR APPLICATION NUMBER: US 60/141,574
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-10-099-99A-21
SSQUENCE 21, Application US/1000999A
Fatent No. 6602980
GENERAL INFORMATION:
TITLE OF INVENTION: SYMTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS
FILE REFERENCE: WEOS-1-1820
CURRENT APPLICATION NUMBER: US/10/009,999A
CURRENT FILING DATE: 1999-10-10
FRIOR FILING DATE: 1999-06-17
FRIOR PELICATION NUMBER: ECT/US99/29357
FRIOR PELICATION NUMBER: US 60/141,574
FRIOR APPLICATION NUMBER: US 60/141,574
FRIOR PELING DATE: 1999-06-17
FRIOR PELING DATE: 1999-06-29
FRIOR PELING DATE: 1999-06-29
FRIOR PELING DATE: 1999-07-02
FRIOR PELING DATE: 1999-07-07
FRIOR PELING DATE: 1999-07-07
FRIOR PELING DATE: 1999-07-07
FRIOR FILING DATE: 1999-07-07
FRIOR FILING DATE: 1999-07-07
FRIOR PELING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PARCHLIN VORS: 45
SEQ ID NOS: 45
SEQ ID NOS: 45
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Fatent No. 6348320
GENERAL INFORMATION:
APPLICANT: EYFE, DAVI
TITLE OF INVENTION: CARTILAGE RESORPTION ASSAYS
FILE REFERENCE: WROS-1-14269
CURRENT APPLICATION NUMBER: US/09/385,740B
CURRENT FILING DATE: 1999-08-30
FRIOR FILING DATE: 1999-07-02
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                                                              FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(7)
CTHER INFORMATION: 6yn-
US-10-073-679-21
              TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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LENGTH: 7
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; LOCATION: (1)..(8)
; OTHER INFORMATION: syn- corr. to N-terminal telopeptide seq. of hu. type II collagen
US-10-073-679-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: PEPTIDE
1 LOCATION: (1)..(8)
1 OTHER INFORMATION: syn- corr. to N-terminal telopeptide seq. of hu. type II collagen
US-10-073-679-22
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US-10-073-679-24

j Sequence 24, Application US/10073679

j Patent No. 6566492

j GENERAL INFORMATION:
APPLICANT: EXTE, David

TILLE OF INVENTION: CARTILAGE RESORPTION ASSAYS
FILE REFERENCE: WROS-1-14269

CURRENT APPLICATION NUMBER: US/10/073,679

CURRENT APPLICATION NUMBER: US/10/073,679

PRIOR APPLICATION NUMBER: US 60/142,274

PRIOR PILING DATE: 1999-08-30

PRIOR PILING DATE: 1999-06-29

PRIOR PILING DATE: 1999-06-29

PRIOR PILING DATE: 1999-06-29

PRIOR PILING DATE: 1999-06-29

PRIOR PILING DATE: 1999-06-29

PRIOR PILING DATE: 1999-06-19

PRIOR PILING DATE: 1999-06-19

PRIOR PILING DATE: 1999-06-19

PRIOR PILING DATE: 1999-06-19

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PATENTIN VETSION 3.0

SEQ ID NO 24
FILE REFERENCE: WROS-1-14269
CURRENT APPLICATION NUMBER: US/10/073,679
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 09/385,740
PRIOR FILING DATE: 1999-08-30
PRIOR FILING DATE: 1999-0-02
PRIOR PILING DATE: 1999-0-02
PRIOR PILING DATE: 1999-0-02
PRIOR PILING DATE: 1999-06-29
PRIOR PILING DATE: 1999-06-29
PRIOR PILING DATE: 1990-06-19
PRIOR PILING DATE: 1990-06-19
PRIOR PILING DATE: 1998-06-19
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 22
LENGTH: 8
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Best Local Similarity 100.
Matches 5; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Gapop 10.0 , Gapext 0.5
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SUMMARIES	115-9 115-9 115-9 115-9 115-9 115-9 115-9 115-9	
IMMA	75-10-615-959- 15-10-615-959- 15-10-615-959- 15-10-073-679- 15-10-615-959- 15-10-615-959- 15-10-615-959- 15-10-073-679- 15-10-073- 15-10-073- 15-10-073- 15-10-073- 15-10-073- 15-10-073- 15-10-073- 15-10-073- 15-10-07	
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ID	1	
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% Query Watch Length DB		
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Score	00000000000000000000000000000000000000	
Result No.	11 22 32 34 44 11 12 13 14 14 15	

Sequence 41, Appl Sequence 23, Appl Sequence 25, Appl Sequence 23, Appl Sequence 25, Appl	22, , 26, 26,	J 4 W W W 4 W	27, 27, 27, 120,	Sequence 28, Appl Sequence 28, Appl Sequence 28, Appl Sequence 123, Appl Sequence 29, Appl Sequence 29, Appl Sequence 29, Appl Sequence 4, Appli
9 12 US-10-615-959-41 9 13 US-10-073-679-23 9 13 US-10-073-679-25 9 14 US-10-408-178-23 9 14 US-10-408-178-23	9 US-09-848-967-2 12 US-10-615-959- 13 US-10-073-679- 14 US-10-408-179- 12 US-10-615-959-	12 US-10-615-959 13 US-10-073-679 14 US-10-408-178 12 US-10-615-959 13 US-10-615-959 13 US-10-615-959	14 US-10-408-178-3 12 US-10-615-959-2 13 US-10-073-679-2 14 US-10-145-012-4 9 US-09-815-877-12	16 12 US-10-615-959-28 16 13 US-10-073-679-28 17 12 US-10-061-78-28 17 12 US-10-615-959-29 17 13 US-10-615-959-29 17 14 US-10-073-679-29 17 15 US-10-073-679-29 17 15 US-10-073-679-29
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## ALIGNMENTS

US-10-615-959-44

US-10-615-959-44

Sequence 44, Application US/10615959

Publication No. US20040048321A1

SEQUENCE 44, David R.

SEQUENCE AL INFORMATION:

APPLICANT: EYE, David R.

TITLE OF INVENTION: SYMTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS

TITLE OF INVENTION NUMBER: US/10/615,959

CURRENT APPLICATION NUMBER: US/10/009,999A

PRIOR PELLING DATE: 1999-12-10

PRIOR APPLICATION NUMBER: US/00/09,999A

PRIOR APPLICATION NUMBER: US/00/09,999A

PRIOR APPLICATION NUMBER: US/01/41,574

PRIOR APPLICATION NUMBER: US/01/41,574

PRIOR PELLING DATE: 1999-06-17

PRIOR PELLING DATE: 1999-07-07

PRIOR PELLING DATE: 1999-07-07

PRIOR PELLING DATE: 1999-07-07

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PRIOR PELLING DATE: 1999-07-07

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PRIOR PELLING DATE: 1999-07-07

PRIOR PELLING DATE: 1999-07-07

PRIOR PEL

Query Match 100.0%; Score 26; DB 12; Length 5; Best Local Similarity 100.0%; Pred. No. 1.2e+06;

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LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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; Sequence 21, Application US/10615959
; Publication No. US20040048321A1
; GENERAL INFORMATION:
    APPLICANT: Eyre, David R.
    TITLE OF INVENTION:
    TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS
    TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS
; TITLE REFERENCE: WROS-1-18220
; CURRENT PILING DATE: 2003-01-08
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US/10/009,999A
; PRIOR FILING DATE: 1999-12-10
; PRIOR FILING DATE: 1999-06-17
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/141,574
; PRIOR FILING DATE: 1999-06-29
; PRIOR FILING DATE: 1999-07-02
; PRIOR FILING DATE: 1999-07-02
; PRIOR FILING DATE: 1999-06-29
; PRIOR FILING DATE: 1999-07-02
                                                                                                                                                                                                                                                                                                                                                                         US-10-615-959-39

Sequence 39, Application US/10615959

Publication No. US20040048321A1

GENERAL INFORMATION:

APPLICANT: Eyre, David R.

TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS

FILE REFERENCE: WROS-1-18220

CURRENT APPLICATION NUMBER: US/10/615,959

CURRENT APPLICATION NUMBER: US/10/009,999A

PRIOR FILING DATE: 2003-07-08

PRIOR FILING DATE: 1999-12-10

PRIOR FILING DATE: 1999-12-10

PRIOR FILING DATE: 1999-66-17

PRIOR FILING DATE: 1999-66-20

PRIOR FILING DATE: 1999-06-20

PRIOR PELLOR DATE: 1999-07-02

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

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PRIOR PELLING DATE: 1999-07-07

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         Mismatches
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             5; Conservative
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LOCATION: (1)..(7) OTHER INFORMATION: syn- corr. to N-terminal telopeptide seq. of hu. type II collagen
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; Sequence 15. Application US/10058124
; Publication No. US20030119058A1
; GENERAL INFORMATION:
; APPLICANT: Ovist, Per
; Bonde, Martin
; TITLE OF INVENTION: A Method for Assaying Collagen Fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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US-10-07-6/7-2.

US-10-07-6/7-2.

US-10-07-6/7-2.

US-10-07-6/7-2.

GENERAL INFORMATION:

APPLICANT: BYTE.

TITLE OF INVENTION: CARTILAGE RESORPTION ASSAYS

FILE REFERENCE: WROS-1-14269

CURRENT APPLICATION NUMBER: 02/36/740

PRIOR APPLICATION NUMBER: 09/385,740

PRIOR PELING DATE: 1999-07-02

PRIOR PELING DATE: 1999-07-02

PRIOR PELING DATE: 1999-06-29

PRIOR PELING DATE: 1999-06-29

PRIOR FILING DATE: 1999-06-17

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PRIOR PRIOR PRIOR DATE: 1999-06-19
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100.0%; Pred. No. 1.2e+06;
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 09/385,740
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.2
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 5; Conservative
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; LOCATION: (1)..(7) $^{\circ} . OTHER INFORMATION: syn- corr. to N-terminal telopeptide seq. of hu. type II collagen US-10-408-178-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22, Application US/10615959

Publication No. US20040048321A1

GENERAL INFORMATION:

APPLICANT: Eyre, David R.

TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS

FILE REFERENCE: WROS-1-18220

CURRENT APPLICANTION NUMBER: US/10/615,959

CURRENT FILING DATE: 2003-07-08

PRIOR FILING DATE: 1999-12-10

PRIOR FILING DATE: 1999-12-10

PRIOR FILING DATE: 1999-12-10

PRIOR APPLICATION NUMBER: US 60/141,574

PRIOR FILING DATE: 1999-06-29

PRIOR FILING DATE: 1999-06-29

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

PRIOR FILING DATE: 1999-07-07

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   PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/335,098
PRIOR PILING DATE: 1999-06-17
PRIOR PILING DATE: 1999-06-19
NUMBER OF SEQ 1D NOS: 31
SOFTWARE: Patentin version 3.0
LENGTH: 7
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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US-10-615-959-24
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                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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in Body Fluids, A Test Kit and Means for Carrying Out the Method and Use of the Method to Diagnose the Presence of Disorders Associated with the Metabolism of
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/058,124

FILING DATE: 29-Jan-2002

CLASSIFICATION: CURROWN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21, Application US/10408178
Fublication No. US20030166032A1
GENERAL INFORMATION:
APPLICANT: EYE, David
TITLE OF INVENTION: CARTILAGE RESORPTION ASSAYS
FILE REFERENCE: WROS.1-14269
CURRENT APPLICATION NUMBER: US/10/408,178
CURRENT FILING DATE: 2003-04-03
FRIOR APPLICATION NUMBER: US/10/073,679
FRIOR APPLICATION NUMBER: 09/385,740
FRIOR FILING DATE: 1999-08-30
FRIOR FILING DATE: 1999-08-30
FRIOR FILING DATE: 1999-07-02
FRIOR APPLICATION NUMBER: US 60/142,274
FRIOR APPLICATION NUMBER: US 60/142,274
FRIOR APPLICATION NUMBER: US 60/142,274
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100.0%; Pred. No. 1.2e+06;
tive 0; Mismatches 0;
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APPLICATION NUMBER: 09/570,573
FILING DATE: 2002-MAY-12
APPLICATION NUMBER: 08/187,319
FILING DATE: cUnknown>
ATTORNEY/ASHT INFORMATION:
NAME: GGODTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 29,714
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
                                                                              NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                      STREET: 805 Third Avenue
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INFORMATION FOR SEQ ID NO: 15:
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                    STATE: New York
                                                                                                                                                                                                                      CITY: New York
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FEATURE: NAME/KEY: MISC_FEATURE
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                                                                                              JOURNALD LINCEMAILURY:

JAPPLICANT: EXFC. David R.

TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS
TITLE REFERENCE: WROS-1-18220
CURRENT APPLICATION NUMBER: US/10/615,959
CURRENT PILING DATE: 2003-01-22
PRIOR FILING DATE: 2003-01-22
PRIOR PELICATION NUMBER: US/10/009,999A
PRIOR FILING DATE: 1999-12-10
PRIOR FILING DATE: 1999-12-10
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 60/141,574
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-08-30
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APPLICANT: BYTE, DAVIG R.

TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS
FILE REPERENCE: WROS-1-1820

CURRENT APPLICATION NUMBER: US/10/615,959

CURRENT FILING DATE: 2003-07-08

PRIOR PELICATION NUMBER: US/10/609,999A

PRIOR PELICATION NUMBER: US/10/609,999A

PRIOR PLING DATE: 1999-12-10

PRIOR PLING DATE: 1999-12-10

PRIOR PLING DATE: 1999-06-17

PRIOR PLING DATE: 1999-06-17

PRIOR PLING DATE: 1999-06-29

PRIOR PLING DATE: 1999-06-29

PRIOR PLING DATE: 1999-06-29

PRIOR PLING DATE: 1999-07-02

PRIOR PLING DATE: 1999-07-02

PRIOR PLING DATE: 1999-07-02

PRIOR PLING DATE: 1999-07-02

PRIOR PLING DATE: 1999-07-02

PRIOR PLING DATE: 1999-07-07

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OTHER INFORMATION: synthetic peptide corresponding to amino-terminal
OTHER INFORMATION: telopeptide sequence of human type II collagen
US-10-615-959-24
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100.0%; Pred. No. 1.2e+06;
iive 0; Mismatches 0;
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; Publication No. US20040048321A1
; GENERAL INFORMATION:
    Sequence 24, Application US/10615959
Publication No. US20040048321A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.2
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Best Local Similarity 100.
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US-10-615-959-40
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KXY: PEPTIDE
LOCATION: (1)..(8)
OTHER INFORMATION: syn- corr. to N-terminal telopeptide seq. of hu. type II collagen
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; OTHER INFORMATION: synthetic peptide corresponding to carboxy-terminal; OTHER INFORMATION: telopeptide sequence of human type III collagen US-10-615-959-40
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                                                                                                                      Length
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GENERAL INFORMATION:

TITLE OF INVENTION: CARTILAGE RESORPTION ASSAYS

FILE REFERENCE: WROS-1-14269
CURRENT APPLICATION NUMBER: US/10/073,679
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/142,274
PRIOR APPLICATION NUMBER: US 60/142,274
PRIOR APPLICATION NUMBER: US 60/141,574
PRIOR APPLICATION NUMBER: US 60/141,574
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-19
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PALENTIN VETSION 3.0
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FILE REFERENCE: WOOS-1-14269
CURRENT APPLICATION NUMBER: US/10/073,679
CURRENT FILING DATE: 2002-02-11
PRIOR PELICATION NUMBER: US 60/142,274
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-07-02
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 60/141,574
PRIOR APPLICATION NUMBER: US 60/141,574
PRIOR APPLICATION NUMBER: US 09/335,098
                                                                                                                   Query Match

100.0%; Score 26; DB 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.2e+06;
Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/10073679 Publication No. US20020182639A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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; LOCATION: (1)..(8)
; OTHER INFORMATION: syn- corr. to N-terminal telopeptide seq. of hu. type II collagen
US-10-408-178-24
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US-10-615-959-23
; Sequence 23. Application US/10615959
; Publication No. US20040048321A1
; GENERAL INFORMATION:
; APPLICANT: Eyre, David R.
; TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR COLLAGEN RESORPTION ASSAYS
; FILE REFERENCE: WROS-1-1820
; CURRENT FILING DATE: 2003-07-09
; CURRENT PILING DATE: 2003-07-09
; RAPICR APPLICATION NUMBER: US/10/009,999A
; PRIOR APPLICATION NUMBER: PCT/US99/29357
; PRIOR PILING DATE: 1999-12-10
; PRIOR PILING DATE: 1999-12-10
; PRIOR PILING DATE: 1999-06-17
; PRIOR PILING DATE: 1999-06-17
; PRIOR PILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 60/141,574
; PRIOR PILING DATE: 1999-06-17
; PRIOR PILING DATE: 1999-07-07
; PRIOR PILING DATE: 1999-07-07
; PRIOR PILING DATE: 1999-07-07
; PRIOR PILING DATE: 1999-07-07
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; PRIOR PILING DATE: 1999-07-07
; PRIOR PILING DATE: 1999-07-07
; PRIOR PILING DATE: 1999-06-30
; RIOR APPLICATION NUMBER: US 60/142,574
; PRIOR PILING DATE: 1999-06-30
; RIOR APPLICATION NUMBER: US 60/142,675
; RIOR PILING DATE: 1999-06-30
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          FILE OF INVENTION: CARTILAGE RESORPTION ASSAYS
FILE REFERENCE: WROS-1-14269
CURRENT APPLICATION NUMER: US/10/408,178
CURRENT FILING DATE: 2003-04-03
PRIOR APPLICATION NUMBER: US/10/073,679
PRIOR APPLICATION NUMBER: US/10/073,679
PRIOR FILING DATE: 1999-08-30
PRIOR FILING DATE: 1999-08-30
PRIOR FILING DATE: 1999-06-29
PRIOR PELLING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 60/141,574
PRIOR PILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: US 60/089,823
PRIOR FILING DATE: 1998-06-19
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PALEGALIN VEREION 3.0
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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NAME/KEY: PEPTIDE
LOCATION: (1)..(8)
OTHER INFORMATION: 8yn- corr. to N-terminal telopeptide seq. of hu. type II collagen
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OTHER INFORMATION: syn- corr. to N-terminal telopeptide seq. of hu. type II collager
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100.0%; Score 26; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels
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| Publication No. USZ0030166032A1
| APPLICATION:
| APPLICATION:
| TITLE OF INVENTION: CARTILAGE RESORPTION ASSAYS
| TITLE OF INVENTION: CARTILAGE RESORPTION ASSAYS
| TITLE REFERENCE: WROS-1-14269
| CURRENT APPLICATION WUMBER: US/10/408,178
| CURRENT FILING DATE: 2003-04-03
| PRIOR FILING DATE: 2002-02-11
| PRIOR APPLICATION NUMBER: US/10/073,679
| PRIOR PILING DATE: 1999-08-30
| PRIOR FILING DATE: 1999-06-29
| PRIOR FILING DATE: 1999-06-29
| PRIOR FILING DATE: 1999-06-29
| PRIOR FILING DATE: 1999-06-29
| PRIOR FILING DATE: 1999-06-17
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100.0%; Pred. No. 1.2e+06;
tive 0; Mismatches 0;
PRIOR FILING DATE: 1999-06-17
PRIOR PEDLICANTON NUMBER: US 60/089,823
PRIOR FILING DATE: 1998-06-19
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.0
SEQ ID NO 24
LENGTH: 8
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Publication No. US20030166032A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 5, Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-10-615-959-25

i Sequence 25. Application US/10615959

publication No. US20040048321A1

GENERAL INFORMATION:

APPLICANT: EVEC. David R.

TITLE REFERENCE: WOSS-1-18220

CURRENT FILING DATE: 2003-07-08

PRIOR PELICATION NUMBER: US/10/615,959

CURRENT FILING DATE: 1999-12-10

PRIOR PELICATION NUMBER: US/10/009,999A

PRIOR PELICATION NUMBER: US/10/009,999A

PRIOR PELICATION NUMBER: US/10/009,999A

PRIOR PELICATION NUMBER: US/10/009,999A

PRIOR PELICATION NUMBER: US/10/009,999A

PRIOR PELICATION NUMBER: US/01-12-10

PRIOR PELICATION NUMBER: US/01/12-14

PRIOR PELICATION NUMBER: US/01/12-14

PRIOR PELICATION NUMBER: US/01/12-14

PRIOR PELICATION NUMBER: US/01/12-14

PRIOR PELICATION NUMBER: US/01/12-14

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OTHER INFORMATION: synthetic peptide corresponding to amino-terminal
OTHER INFORMATION: telopeptide sequence of human type II collagen
US-10-615-959-25
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100.0%; Score 26; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels
Query Match
100.0%; Score 26; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels
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Search completed: September 18, 2004, 04:56:16 Job time : 25.7255 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

sw model OM protein - protein search, using Run on:

September 18, 2004, 04:02:05; Search time 6.07843 Seconds (without alignments) 79.125 Million cell updates/sec

US-10-615-959-44 26 1 EKAGG S Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_78:\* Database :

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	Qi	7	H97716	AH1056	A11951	T31248	S18397	B90439	AB3014	E98270	S22357	H70441	C97823	AB3349	G95343	D38257	E38257	C81886	B81135	D85636	B64842	C88473	A45029	539863	\$18250	D87724	T33051	E83816	F71002	G75128
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* Query	Match	100.0	100.0	100.0	100.0	100.0	100.0		100.0	100.0	100.0	100.0	100.0		100.0	100.0	100.0	100.0	100.0	100.0	100.0		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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ribonuclease III h	ribonuclease III h	tumor necrosis fac	phosphoglycolate p	extragenic suppres	phosphodlycolate p	glucan endo-1,3-be	probable fructose-	hypothetical prote	hypothetical prote	qlucan endo-1,3-be	polymerase-associa	probable zinc find	hypothetical prote	glucan endo-1,3-be	conserved hypothet	
AE1300	AE1672	S24642	AB2775	D69546	H97554	T45802	H81356	F64306	T19954	C38257	S20830	G86143	H75091	JC1439	F72255	ALIGNMENTS
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229	229	233	233	252	265	278	280	281	293	298	299	304	305	317	318	
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26	56	56	56	26	56	56	56	56	56	56	56	56	56	56	56	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

505 ribosomal protein L28 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Species: Rickettsia conorii
C;Species: Rickettsia conorii
C;Species: Bate: 30-58p-2001
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, I.
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, I.
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Recession: H9774
A;Recession: H9774
A;Status: preliminary
A;Accession: H9774
A;Accession: H9774
A;Residues: 1-97 «KUR»
A;Residues: 1-97 «KUR»
A;Cross-references: GB:AE006914; PIDN:AAL02674.1; PID:g15619179; GSPDB:GN00173
A;Genetics:
A;Genetics:

D.; ROL

Gaps .; 0 Query Match 100.0%; Score 26; DB 2; Length 97; Best Local Similarity 100.0%; Pred. No. 87; Matches 5; Conservative 0; Mismatches 0; Indels

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A,Accession: T11248
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
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A; Accession: B90439
A; Reference number: Z20992
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Best Local Similarity
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                                                                                                                                                                                              A; Genome: plasmid pNL1
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Matches
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Matches
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A11951
hypothetical protein alli164 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Accession: A11951
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi RARazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CiAccession: T31248
RiRomine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; G submitted to the EMBL Data Library, July 1998
A;Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromati
                                                                                                                          hypothetical protein STY4780 [imported] - Salmonella enterica subsp. enterica serovar Typhi G;Species: Salmonella enterica subsp. enterica serovar Typhi G;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi G;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 G;Accession: AH1056 R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R; Pickard, D.; Wain, J; Churcher, F; Connerton, P; Cronin, A; Davis, P; Davies, R.M; Dowd, L; White, N.; Farrar, S; Moule, S; OʻGaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Althors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
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A;Residues: 1-120 <PAR>
A;Crosales-references: GB:AL513382; PIDN:CAD06901.1; PID:g16505549; GSPDB:GN00176
C;Genetics:
A;Gene: STY4780
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A;Rosidues: 1-126 <KUR>
A;Rosirates: 1-126 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB73121.1; PID:g17130510; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
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T31248
T31248
Cj.Pecies Sphingomonas aromaticivorans plasmid pNL1
Cj.Species: Sphingomonas aromaticivorans
Cj.Species: Sphingomonas aromaticivorans
Cj.Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
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Best Local Similarity 100.
Matches 5; Conservative
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Matches 5; Conserv
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C,Accession: S18397
R;Piccinini, M.; Kleinschmidt, T.; Gorr, T.; Weber, R.E.; Kuenzle, H.; Braunitzer, G.
R;Piccinini, M.; Kleinschmidt, T.; Gorr, T.; Weber, R.E.; Kuenzle, H.; Braunitzer, G.
A;Title: Primary structure and oxygen-binding properties of the hemoglobin from the lesse A;Reference number: S18397; MUID:92172283; PMID:1793518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-v. Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. Surrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A; Description: Sulfolobus solfataricus complete genome.
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A;Residues: 1-145 <KUR>
A;Cross-references: GB:AE006641; NID:g13815963; PIDN:AAK42769.1; GSPDB:GN00155
A;Residues: 1-130 <ROM>
A;Cross-references: EMBL:AF079317; NID:g3378261; PID:g3378389; PIDN:AAD03972.1
C;Genetics:
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A;Status: precent type: protein
A;Residues: 1-141 <PIC>
C;Superfamily: globin; globin homology
C;Superfamily: globin; globin homology
C;Keywords: blood; chromoprotein; heme; iron; metalloprotein; oxygen carrier
F;2-141/Domain: globin homology <GLS>
F;87/Binding site: heme iron (His) (proximal axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hemoglobin alpha chain - small Madagascar hedgehog
C;Species: Echinops telfairi (small Madagascar hedgehog)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 19-May-2000
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C,Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
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100.0%; Score 26; DB 2; 1
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                      Similarity 100.0%; Score 26; DB 2; I Similarity 100.0%; Pred. No. 1.1e+02; 5; Conservative 0; Mismatches 0;
                                                                                                                                                                             A;Note: orf942
C;Superfamily: hypothetical protein H10719
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61

EKAGG

57

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Rili, H.; Subar, M.; Lee, K.M.; Boussios, T.
Biochim. Biophys. Acta 1130, 218-220, 1992
A;Title: Cloning and sequence analysis of two embryonic beta-like globin cDNAs (y and z)
A;Title: Cloning and sequence analysis of two embryonic beta-like globin cDNAs (y and z)
A;Accession: S22356; MUID:92223098; PMID:1339291
A;Accession: S22357
A;Accession: S2356; MUID:949617; PIDN:CAA45518.1; PID:949618
A;Status: preliminary
A;Residues: 1-147 < LIH>
A;Cross-references: EMBL:X64179; NID:949617; PIDN:CAA45518.1; PID:949618
A;Cross-references: EMBL:X64179; Mexiding of Carrier
C;Superfamily: globin, homology
C;Reywords: chromoprotein, homology cGLB>
F;4-147/Domain: globin, homology cGLB>
F;4-147/Domain: globin, homology cGLB>
F;4-147/Domain: globin, distal axial ligand) #status predicted
F;93/Binding site: oxygen (His) (proximal axial ligand) #status predicted
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A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
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C;Species: Rickettsia conorii
C;Species: Rickettsia conorii
C;Accession: C97823
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
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A,Reference number: A70300, MUID:98196666, PMID:9537320
A,Accession: H70441
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C;Date: 08-May.1998 #sequence_revision 08-May-1998 #text_change 13-Aug-1999
C;Accession: H70441
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100.0%; Score 26; DB 2; Length 147;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels
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C;Superfamily: Escherichia coli ribosomal protein L15
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C;Superfamily: Escherichia coli ribosomal protein L15
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                                                                                                                                                                                                                                                                                                                              Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                 conserved hypothetical protein Atu3718 [imported] - Agrobacterium tumefaciens (strain C5 C; Species: Agrobacterium tumefaciens C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002 C; Accession: AB3014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pypothetical protein AGR L 2234 [imported] - Agrobacterium tumefaciens (strain C58, Cere Cispecies: Agrobacterium tumefaciens
Cispecies: Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
Ciscession: E98270
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ster, E.W.
A,Tille: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
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A;Experimental source: strain C58 (Dupont)
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C;Species: Mesocricetus auratus (golden hamster)
C;Date: 22-Nov-1993 #sequence_revision 01-bec-1995 #text_change 04-Mar-2000
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Query Match 100.0%; Score 26; DB 2; I Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 5; Conservative 0; Mismatches 0;

97 EKAGG 101

A,Map position: linear chromosome C,Superfamily: 15.5K protein (tolAB operon 5' region)

A; Gene: Atu3718

C; Genetics:

A; Residues: 1-146 < KUR>

A; Molecule type: DNA

Status: preliminary

Indels

0; Mismatches

Local Similarity 100.

Best Loc Matches

Query Match

97 EKAGG 101

RESULT 10

1 EKAGG 5

A,Gene: AGR L 2234 A;Map position: linear chromosome C;Superfamily: 15.5K protein (tolAB operon 5' region)

1-146 <KUR>

C, Genetics:

A;Accession: E98270 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-146 <KUR

Gaps

0;

Indels

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Mismatches

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glucan endo-1,3-beta-D-glucosidase (EC 3.2.1.39), acidic (clone c130) - common tobacco (c
                                                                                                                                                                                                                                                                                                                 Cispecies: Nicotiana tabacum (common tobacco)
Cibate: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 13-Sep-1998
Cipate: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 13-Sep-1998
Cipacession: D38257
Rilinthorst, HJ.M.; Melchers, L.S.; Mayer, A.; Van Roekel, J.S.C.; Cornelissen, B.J.C.;
Proc. Natl. Acad. Sci. U.S.A. 87, 8756-8760, 1990
A; Ritle: Analysis of gene families encoding acidic and basic beta-1,3-glucanases of tobac A; Recession: D38257
A; Recession: D38257
A; Accession: D38257
A; Status: preliminary; not compared with conceptual translation
A; Molecule Type: mRNA
A; Residues: 1-162 < LIN>
C; Superfamily: beta-1,3-glucanase
C; Keywords: glycosidase; hydrolase; polysaccharide degradation
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A; Accession: '05343
A; Retatus: preliminary
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A; Retatus: preliminary
A; Retatus: preliminary
A; Residues: '1-15 «KUR»
A; Forsa references: GB: AE006469; PIDN: AAK65313.1; PID: g14523769; GSPDB: GN00165
A; Experimental source: gtrain 1021, megaplasmid pSymA
A; Galibert, F; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
P; F; Finan, T.M.; Jones, T.
C.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A; Contents: annotation
C; Genetics:
A; Gene: SMall200
A; Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                          LSU ribosomal protein LISP [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C;Cacession: AB3349
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein SMa1200 [imported] - Sinorhizobium meliloti (strain 1021) magaplasm
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug_2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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**Saznet, M.J; Pisher, T.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
**Saznet, M.J; Pisher, R.F.; Jones, T.; Komp, C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
**Froc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
**Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
**A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot
**A;Reference number: A95262; MUID:21396509; PMID:11481432
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tive 0; Mismatches 0;
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A; Map position:
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 18, 2004, 03:48:54; Search time 3.72549 Seconds (without alignments) 69.884 Million cell updates/sec Run on:

US-10-615-959-44 26 1 EKAGG 5

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	092jdl rickettsia 924291 echinops te P29429 echinops te P29426 mesocricetu 067561 aquifex aeo P52397 nicotiana t 09xd17 leptospira P42791 arabidopsis 0896b5 bifidobacte 084x44 escherichia P30849 escherichia P30849 escherichia P30849 escherichia P30849 escherichia P30849 escherichia P30849 bacillus su 092ax3 listeria mo 08yd91 listeria mo 08yd91 listeria mo 08yd91 listeria mo 08bey agrobacteri 006599 bos taurus P59684 bos indicus P59684 bos indicus P59684 bos indicus P59684 bos indicus P59684 bos indicus P59684 bos indicus P59684 bos indicus P5339 micotiana t 060139 methanococc 088mb9 pseudomonas P60168 mesales vir 09hih c thermoplasm 002439 hordeum vul P36520 saccharomyc P5332 saccharomyc P5332 saccharomyc P5332 saccharomyc P55332 saccharomyc P95332 saccharomyc P69199 ovis aries	
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Query Match
100.0%; Score 26, DB 1, Length 97,
Best Local Similarity 100.0%; Pred. No. 34,
Matches 5; Conservative 0; Mismatches 0; Indels

RESULT 2
RL28\_RICPR
ID RL28\_RICPR STANDARD; PRT; 97 AA. AC 092E48;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)

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P00636 sus scrofa P00637 oryctolagus P23547 nicotiana t Q03773 glycine max P52408 prunus pers P23432 nicotiana t P23433 nicotiana t P53399 nicotiana t P19112 rattus norv Q990m6 homo sapien Q8ram9 thermoanaer Q20252 spinacia ol		Rickettsiales;	nier PE., Barbe V., , Claverie JM., and R. prowazekii.";	OT entry is copyright. It is produced through a collaboration Swiss Institute of Bioinformatics and the EMBL outstation. Swiss Institute of Bioinformatics and the EMBL outstation. Bloinformatics institute. There are no restrictions on its profit institutions as long as its content is in no way this statement is not removed. Usage by and for commercial lites a license agreement (See http://www.isb-sib.ch/announce/ail to license@isb-sib.ch).  (b. AAL02674.1;
F16P_PIG F16P_RABIT B13G_TOBAC B13A_SOYEN B13A_SOYEN E13A_TOBAC B13D_TOBAC E13D_TOBAC F16P_RAT H2AW_HUMAN TGT_THETN	ALIGNMENTS PRT: 97 AA	uence updat lotation upd laproteobact	., Four bach J. conorii	Ty is copyright. It is produced Institute of Bioinformatics and Ormatics Institute. There are institutions as long as its tratement is not removed. Usage license agreement (See http://r.licenseaisb-sib.ch).  1. Ribosomal L28.  7. Ribosomal L28.  1. Complete proteome.  Complete proteome.
100.0 337 1 100.0 343 1 100.0 343 1 100.0 351 1 100.0 351 1 100.0 351 1 100.0 351 1 100.0 351 1 100.0 351 1 100.0 351 1 100.0 371 1	STANDARD;	(Rel. 41, Created) (Rel. 41, Last sec (Rel. 41, Last and L protein L28. 6. Norii. Sechacteria; Alph Re; Rickettsieae;	SECENCE FROM N.A. STRAIN=Malish 7; MEDININE=21442074; PubMed=11557893; Ogata H., Audic S., Renesto-Audiffren P. Samson D., Roux V., Cossart P., Weissenf. Raoult D.; Whechanisms of evolution in Rickettsia ( Science 293:2093-2098(2001).	This SWISS-PROT entry is copyright. It between the Swiss Institute of Bioinfor the European Baoinformatics Institute. Use by non-profit institutions as lo modified and this statement is not remoenties requires a license agreement or send an email to license@isb-sib.ch) EMBL, AE008580; AAL02674.1;
335 26 11 33 35 35 35 35 35 35 35 35 35 35 35 35	RESULT 1 RL28_RICCN ID FRL28 RICCN	Q92JD1; 28-FEB-2003 (Rel. 41, C28-FEB-2003 (Rel. 41, I) 28-FEB-2003 (Rel. 41, I) 50S ribosomal protein I RPMB OR RC0136. Rickettsia conorii. Bacteria; Proteobacteri Rickettsiaceae; Rickettsiaceae; Rickettsiaceae; NCBI_TaxID=781;	SEQUENCE FROM N STRAIN=Malish 7 MEDLINE=2144207 Ogata H., Audio Samson D., Roux Raoult D.; "Mechanisms of Science 293:209	This SWISS-PROT between the Swi the European Bi use by non-proc modified and thi entities require or send an email EMBL, AE008580; PR, H97716; H97 HAMAP; MF 03739; InterPro; IPR001 Pfam; PF00830; R TICRFAMS; TIGROD Ribosomal protei
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100.0%; Score 26; DB 1; Length 141; 100.0%; Pred. No. 48;
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METAL 58 1RON (HEME DISTAL LIGAND).
METAL 78 97 1RON (HEME PROXIMAL LIGAND).
SEQUENCE 141 AA; 15027 MW; 379F8241EC1E9D29 CRC64;
             -i- TISSUE SPECIFICITY: Red blood cells.
-i- SIMILARITY: Belongs to the globin family.
PIR, 518397, 518397.
HSSP: PO1558; ZMIB.
INTERPRO: PRO02338; Alpha haem.
InterPro: IPR000971; Globin.
                                                                                                                                                                                                                                                                                                              0; Mismatches
           SPECIFICITY: Red blood cells.
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                                                                                                                         Pfam; PF00042; globin; 1.
PRINTS; PR00612; ALPHAHAEM.
PROSITE; PS01033; GLOBIN; 1.
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                        SEQUENCE
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Biol. Chem. Hoppe-Seyler 372:975-98(1991).
-!-FUNCTION: Involved in oxygen transport from the lung to the various peripheral tissues.
-!-SUBUNIT: Heterotteramer of two alpha chains and two beta chains.
Two external cysteine residues at beta-16 and beta-52 cause reversible polymerization to octamers and most likely irreversible formation of higher polymers.
                                                                                                                                                                                               MEDLINE=99039499; PubMed=9823893; Andersson J.O., Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of mitochondria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Echinops telfairi (Lesser hedgehog tenrec).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Insectivora, Tenrecidae, Tenrecinae, Echinops.
                                                                                                                                                                                                                                                                                                                        Nature 396:133-140(1998).
-!- SIMILARITY: Belongs to the L28P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92172283; PubMed=1793518;
Piccinini M., Kleinschmidt T., Gorr T., Weber R.E., Kuenzle H.,
Braunitzer G.;
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0
                                                                            Rickettaia prowazekii.
Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Rickettsiaceae, Rickettsieae, Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 26; DB 1; Length 97; 100.0%; Pred. No. 34; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96889B2F4E1E28C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1992 (Rel. 21, Created) 01-MAR-1992 (Rel. 21, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Hemoglobin alpha chain.
50S ribosomal protein L28. RPMB OR RP099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ribosomal protein, Complete proteome SEQUENCE 97 AA; 10953 MW; 96889B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP, MF 00373; -; 1.
InterPro; IPR001383; Ribosomal L28.
Pfam; PF00830; Ribosomal L28; 1.
TIGRFAMS; TIGR00009; L28; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ235270; CAA14569.1; -.
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Matches 5; Conservative
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                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                  NCBI_TaxID=782;
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P24291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochim. Biophys. Acta 1130:218-220(1992).
-I- FUNCTION: This is a minor early embryonic beta chain.
-i- SUBUNIT: Heterotetramer of two alpha chains and two beta chains.
-i- SIMILARITY: Belongs to the globin family.
                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=92223098; PubMed=1339291;
MEDLINE=92223098; PubMed=1339291;
MEDLINE=92223098; PubMed=1339291;
MEDLINE=92223098; Lee K.M., Boussios T.;
"Cloning and sequence analysis of two embryonic beta-like globin cDNAs (Y and z) of hamster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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INIT MET 0 0 BY SIMILARITY.
METAL 63 63 IRON (HEME DISTAL LIGAND)
METAL 92 92 IRON (HEME PROXIMAL LIGAND).
SEQUENCE 146 AA, 16274 MW, 2E7D0D46898DFF4F CRC64;
                                                                  01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
28-FBS-2003 (Rel. 41, Last annotation update)
Hemoglobin beta-Y chain.
146 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                        Mesocricetus auratus (Golden hamster).
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InterPro; IPR00337; Beta haem.
InterPro; IPR000971; Globin.
Pfam; PF00042; globin; 1.
PRINTS; PR00814; BETAHAEM.
PROSITE; PS01033; GLOBIN; 1.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
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135 12
160 AA;
                                                                                                                                                                                                                                                                                                                                            Vandekerckhove J.;
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                                             NCBI_TaxID=4097;
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ACT SITE
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                                                                                                                                                                                                                                                                                                                                                                                                               system."
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  AX OOS BELL BY SX OOS BELL BY SX OOS BELL BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY SX OOS BY S
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01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
610-0CT-2001 (Rel. 40, Last annotation update)
610-0CT-2001 (Rel. 40, Last annotation update)
610-31-beta-glucan endohydrolase) ((1->3)-beta-glucanase) (Beta-1,3-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aljay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: This protein binds directly to 23S ribosomal RNA (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
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                                                                                                                                                                                                                                                                                                                                                 Bacteria, Aquificae, Aquificales, Aquificaceae, Aquifex.
NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Complete proteome.
12BBDA4E92D90357 CRC64;
                                                                                                                                                                                                                        30-MAX'-2000 (Rel. 39, Created)
30-MAY'-2000 (Rel. 39, Last sequence update)
30-CCT-2001 (Rel. 40, Last annotation update)
50S ribosomal protein 115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRFAMS; TIGRO1071; Tp10 bact; 1.
PROSTIE; PROSU475; RIBOSOWAL L15; PRLSE NEG.
Ribosomal protein; TRNA-binding; Complète p
SEQUENCE 149 AA; 16572 MM; 12BBDA4592D9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000749; AAC07532.1; -.
PIR; H70441; H70441;
InterPro; IPR001196; Ribosomal L15.
InterPro; IPR005749; Ribosomal_L15_b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nicotiana tabacum (Common tobacco)
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Pfam; PF01305; Ribosomal_L15; 1.
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                EKAGG 25
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                          EKAGG 5
                                                                                                                                                                                                                                                                                                                                          Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                    RPLO OR AQ 1642.
                                                                                                                                  RESULT 5
RL15_AQUAE
ID RL15_AQUAE
AC 067561;
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ID _E13J_TOBAC
AC P52397;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in 1,3-beta-D-glucans.
--- SUBCELLULAR LOCATION: Extracellular.
--- INDUCTION: Not found in healthy tissues, but accumulates to high levels in the extracellular compartment of leaves in response to pathogen infection or treatment with salicylic acid.
--- PTM: The N-terminus is blocked.
--- SIMILARITY: Belongs to family 17 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 86:2673-2677(1989).
-!- FUNCTION: Implicated in the defense of plants against pathogens.
-!- CATALYTIC ACTIVITY: Hydrolysis of 1,3-beta-D-glucosidic linkages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Characterization of vacuolar and extracellular beta(1,3)-glucanases of tobacco: evidence for a strictly compartmentalized plant defense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
                                                                                                                                                                                                                                                                   "Differential regulation of beta-1,3-glucanase messenger RNAs in response to pathogen infection."; Plant Physiol. 96:390-397(1991).
                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-ECY. XENTELING; TISSUE-Least;
WARD E.R., PAYNE G.B., MOYER M.B., Williams S.C., Dincher S.S.,
Sharkey K.C., Beck J.J., Taylor H.T., Ahl-Goy P., Meins F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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Pred. No. 55;
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 70-93; 126-136; 143-152 AND 155-160.
van den Bulcke M., Bauw G., Castresana C., van Montagu M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTON DONOR (BY SIMILARI'
A -> N (IN REF. 2).
K -> Q (IN REF. 2).
; 98C270F390764B7F CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
So ribosomal protein L15.
RPLO OR LA0758.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 AA.
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lamiids; Solanales; Solanaceae; Nicotiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro, IPR000490, Glyco_hydro_17.
Bern, PR00132; Glyco_hydro_17, 1.
PR05ITE; PS00587; GlYCOSYL, HYDROL F17; 1.
Hydrolase, Glycosidase; Multigene_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17980 MW;
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Best Local Similarity luv...
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                               A Salanoubat M., Lemcker H., Perez-Alonso M., Obermaier B., Ratrmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B., Balanoubat M., Lemcker H., Perez-Alonso M., Obermaier B., Belseny M., Boutry M., Grivell L.A., Macher R., Puigdomench P., Robert C., Brottier P., Ra Besimone V., Choisne N., Ariguenave F., Robert C., Brottier P., Ra Gabefer M., Muellar-Auer S., Gabel C., Fuchs M., Benes V., Murcher E., Drzonek H., Eride H., Jordan N., Bangert S., Murmbach E., Drzonek H., Voss H., Holland R., Brandt P., Nyakatura G., Ra Wurmbach E., Drzonek H., Voss H., Holland R., Brandt P., Nyakatura G., Ra Wurmbach E., Drzonek H., Schoen O., Bargues M., Terol J., Climent J., Raichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J., Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J., Ravarro P., Collado C., Perez-Perez A., Otterwaelder B., Duchemin D., Ray Mararo P., Argirtou A., Flores M., Liguori R., Vitale D., Mannbaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W., Rannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Marander J., Sellers P., Gill J.E., Feldblyum T.V., Rrack M., Mattis R., Wu D., Peterson J., Van Aken S., Rater T., Nieman M.C., Salzberg S.L., Mitte O., Venteer J., C., Venteer J., Kaneko T., Nakaman M.C., Salzberg S.L., Muraki A., Kaneko T., Nakaman M.C., Salzberg S.L., Muraki A., Kaneko T., Nakaman M.C., Salzberg S.L., Muraki A., Kaneko T., Nakaman M.C., Salzberg S.L., Muraki A., Kaneko T., Nakaman M.C., Salzberg S.L., Muraki A., Matanabe A., Yamada M., Yasuda M., Tabata S., Nakazaki M., Yasuda M., Tabata S., Nakazaki M., Yasuda M., Tabata S., Nakazaki M., Yasuda M., Tabata S., Nakazaki M., Yasuda M., Tabata S., Nakazaki M., Yasuda M., Tabata S., Nakazaki M., Yasuda M., Tabata S., Takeuchi C., Wada T., Halling M., Palisan M., Palisan S., Nakazaki M., Yasuda M., Tabata S., Nakazaki M., Yasuda M., Tabata S., Takeuchi C., Wada J., Halling M., Tabata S., Nakazaki M., Yasuda M., Tabata S., Takeuchi C., Wada J., Halling M., Mattanabe A., Yasuda M., Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CV. COlumbia;

K MEDLINE=22954850; PubMed=14593172;

K MEDLINE=22954850; PubMed=14593172;

Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,

Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

A Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Tariumi M.J.,

Chan M.M., Tang C.C., Condera C.S., Deng J.M., Akiyama K., Ansari Y.,

A Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

A Chao Q., Choy W., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,

A Hayshizaki Y., Johnson-Hopson C., Hsuan V.W., Lida K., Karnes M.,

Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

A Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

A Xuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,

"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 302:842-846(2003).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the L18E family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfan; PF00828; Ribosomal L18e; 1.
PROSITE; PS01106; RIBOSOMAL L18E; FALSE NEG.
Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro; IPR000039; Ribosomal_L18e.
                                                                                                                                                      STRAIN=cv. Columbia;
MEDLINE=21016720; PubMed=11130713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AC011620; AAF26138.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AY060533; AAL31164.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U15741; AAA69928.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 408:820-822(2000).
                                    Gene 153:171-174(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                 SECUENCE FROM N.A
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                                                                                                                                                                                                                                                               [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=22588143; PubMed=12712204;
Ren S.-X., Fu G., Jiang X.-G., Zeng R., Mido Y.-G., Xu H.,
Ren S.-X., Fu G., Jiang X.-G., Zeng R., Mido Y.-G., Yi H.,
Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
Jiang J.-X., Gu W.-Y., Zhang Y.-O., Cai Z., Sheng H.-H., Yin H.-F.,
Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
Yao Z.-J., Shen Y., Oxnoralle R.L., Wen Y.-M., Shi M.-H., Chen Z.,
Xu J.-G., Zhao G.-P.,
"Unique physiological and pathogenic features of Leptospira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=cv. Columbia;
MEDLINE=95180713; PubMed=7875584;
Baima S., Sessa G., Ruberti I., Morelli G.;
"A cDNA encoding Arabidopsis thaliana cytoplasmic ribosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interrogans revealed by whole-genome sequencing.";
Nature 422:888-893(2003)
-!- FUNCTION: This protein binds directly to 23S ribosomal RNA (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
-!- SIMILARITY: Belongs to the L15P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                STRAIN=Lai / Serogroup Icterohaemorrhagiae / Serovar lai;
MEDINE=20088835; PtubMed=10620683;
Juerner R.L., Hartskeerl R.A., van de Kemp H., Bal A.E.;
"Characterization of the Leptospira interrogans S10-spc-alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 26; DB 1; Length 180; 100.0%; Pred. No. 61; or Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2B9D951F905A0602 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPL18 OR AT3G05590 OR F18C1.14.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                               FEMS Microbiol. Lett. 182:303-308(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE011262; AAN47957.1; -.
InterPro, IPR001196; Ribosomal L15.
InterPro, IPR005749; Ribosomal L15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF115283; AAD40602.1; -.
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SEQUENCE FROM N.A.
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Matches

셤

RESULT 8
RIB ARATI
ID ARATI
ID ARATI
ID 28-8
DT 28-8
DT 28-8
DT 28-8
DT 28-8
CO EUKA
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WRBA_ECO57
       RESULT 10
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                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The genome sequence of Bifidobacterium longum reflects its adaptation to the human gastrointestinal tract.";

Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).

-!- FUNCTION: Catalyzes a salvage reaction resulting in the formation of AMP, that is energically less costly than de novo synthesis.

-!- CATALYTIC ACTIVITY: AMP + diphosphate = adenine + 5-phospho-alpha-
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pram; Frvasov, ...
TIGREMAS, TIGRO1090; apt, 1.
PROSITE; PS00103: PUR_PYR_PR_TRANSFER; 1.
Transferase; Glycysyltransferase; Purine salvage; Complete proteome.
Transferase; Glycysyltransferase; Purine salvage; Complete proteome.
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0
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Bifidobacteriaceae; Bifidobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22294977; PubMed=12381787; Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B., Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M., Pridmore R.D., Arigoni F.;
                                                   100.0%; Score 26; DB 1; Length 187; 100.0%; Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 26; DB 1; Length 193; 100.0%; Pred. No. 65;
                                                                                        0; Indels
   59 K -> R (IN REF. 1).
20926 MW; DDC72C02B12CBCBB CRC64;
                                                                                                                                                                                                                                                                      15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Adenine phosphoribosyltransferase (EC 2.4.2.7) (APRT).
APT OR BL0731.
Bifidobacterium longum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP, MF_00004; -; 1.
InterPro; IPR005764; Ade phspho_trans.
InterPro; IPR002375; Pr/py_rp_transf.
InterPro; IPR000836; PRTransferase.
Pfam; PF00156; Pribosyltran; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE014695; AAN24548.1; -.
                                                                                        Conservative
                                                                                                                                                                                                                                          STANDARD;
59
187 AA;
                                                                   Local Similarity
les 5; Conserv
                                                                                                                                                      113 EKAGG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=216816;
                                                                                                                      1 EKAGG 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=NCC 2705;
                                                                                                                                                                                                                                        APT_BIFLO
Q8GGB5;
   CONFLICT
                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156211; PubMed=11258796;
MEDLINE=21156211; PubMed=11258796;
MEDLINE=21156211; PubMed=11258796;
Han C.-G., Ohtsubo R., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.,
"Complete genome sequence of enterohemorrhagic Escherichia coli
"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Res. 8:11-22 (2001).

-!- FUNCTION: Seems to enhance the formation and/or stability of norovalant complexes between the trp repressor protein and operator-bearing DNA (By similarity).

-!- COFACTOR: Binds 1 FMN per monomer (By similarity).

-!- SIMILARITY: Belongs to the wrbA family.

-!- SIMILARITY: Contains 1 flavodoxin-like domain.

-!- CAUTION: WrbA is interrupted by the insertion of the prophage VT2-Sakai between positions 17 and 18.
                                                                                                                                                                                                                                                                                               MEDLINE=20198780; PubMed=10734605; MEDLINE=20198780; PubMed=10734605; Makino K., Yokoyama K., Kubota Y., Yutsudo C.H., Kimura S., Makino K., Yokoyama K., Hattori M., Tatsuno I., Abe H., Iida T., Yamamoto K., Ohnishi M., Hayashi T., Yasunaga T., Honda T., Sasakawa C., Shinagawa H.; Yasunaga T., Honda T., Complete nucleotide sequence of the prophage VT2-Sakai carrying the "Complete nucleotide sequence of the prophage VT2-Sakai carrying the derived from the Sakai outbreak.", Genes Genet. Syst. 74:227-239(1999),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-21074935; PubMed-11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Bosfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
"Genome sequence of enerchaemorrhagic Escherichia coli O157:H7.";
                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
WRBA ECOS7 STANDARD, PRT; 197 AA. 08X4B4; Q8X468; Q9XXH7; 28-FEB-2003 (Rel. 41, Created) 26-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Flavoprotein wrba (Trp repressor binding protein). WRBA OR Z1423/Z1504 OR ECS1159.1/ECS1251.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=0157:H7 / EDL933 / ATCC 700927;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AE005294; AAG55552.1; ALT_INIT.
EMBL, AE005300; AAG55621.1; ALT_TERM.
EMBL, AP002554; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                              Enterobacteriaceae; Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 409:529-533 (2001).
                                                                                                                                                                 Escherichia coli 0157:H7
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                    NCBI_TaxID=83334;
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Gaps

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0; Indels

0; Mismatches

5; Conservative

Matches

156 EKAGG 160

1 EKAGG 5

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WEDLINE=22388234; PubMed=12471157;

WEDLINE=22388234; PubMed=12471157;

WEDLINE=22388234; PubMed=12471157;

WEDLINE=22388234; PubMed=12471157;

WEDLINE=2388234; PubMed=12471157;

Maskew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extransive mosaic structure revealed by the complete genome sequence

of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIESE CO11; STRAIN=K12;
MEDLINE=97061202; PubMed=8905212;
OBhima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Isemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278803;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Maybew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yano M., Horiuchi T.; "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
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0
                                                                            100.0%; Score 26; DB 1; Length 197; 100.0%; Pred. No. 66; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose
Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
           Flavorotein; FMN; Complete proteome.

INIT MET 0 0 BY SIMILARITY.

DOMAIN 3 188 FLAVODOXIN-LIKE.

SEQUENCE 197 AA; 20703 MW; 7117EF93D3B72447 CRC64;
                                                                                                                                                                                                                                        P30849; P75890; P77543;
01-JUL-1993 (Rel. 26, Created)
10-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Flavoprocein wrbA (Trp repressor binding protein)
WRBA OR B1004 OR C1140 OR SF1008 OR S1077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 90:5796-5800(1993)
                                                                                                                                                                                                                             197 AA
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 1-18.
SPECIES=E.coli; STRAIN=K12;
MEDLINE=93296226; PubMed=8516330;
PROSITE; PS50902; FLAVODOXIN_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                            Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=562, 217992, 623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                      Escherichia coli,
Escherichia coli 06, and
Shigella flexneri.
                                                                                                         5; Conservative
                                                                                                                                                                                                                              STANDARD;
                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                           48 EKAGG 52
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XX MEDLINE=22590274; PubMed=12704152;
XX MEDLINE=22590274; PubMed=12704152;
XX MEDLINE=22590274; PubMed=12704152;
XX Wei J., Goldberg M.B., Burland V., Venkateean M.M., Deng W.,
XX Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
XX Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
XX Mantiz D.C., Blattner F.R.;
XX Tomplete genome sequence a457T.";
XX Tomplete genome sequence a457T.";
XX Tomplete genome sequence a457T.";
XX Tomplete genome sequence the ferral comparative genomics of Shigella
XX Tomplete genome sequence a457T.";
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XX Tomplete genome 
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Biochemical characterization of WrbA, founding member of a new family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=S.flexmeri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                         SPECIES=E.coli; STRAIN=JM101;
MEDLINE=98361966; PubMed=9694845;
Grandori R., Khalifah P., Boice J.A., Fairman R., Giovanielli K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of multimeric flavodoxin-like proteins.";
J. Biol. Chem. 273:20960-20966(1998).
[5] SEQUENCE OF 1-10, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; _IPR008254; Flav_nitox_synth.
InterPro; IPR001226; Flavodoxin.
Pfam; PF00258; flavodoxin; 1.
PROSITE; PS50902; FLAVODOXIN_LIKE; 1.
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EMBL; D90737; BAA35771.1; --
EMBL; AB016758; AAN79608.1; --
EMBL; AB015129; AAN42634.1; --
EMBL; AB016981; AAN42634.1; --
EMBL; AB016981; AAN42634.1; --
EMBL; AB016981; AAN42634.1; --
EMBL; AB016981; AAN42634.1; --
EMBL; AB016981; AAN42634.1; --
EMBL; AB016981; AAN42634.1; --
EMBL; AB0482; B64842; --
EMBL; AB0482; --
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EMBL; AE000202; AAC74089.1; -.
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EcoGene; EG11540; wrbA.
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HAMAP; MF_01017;
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Kratzin H., Yang C.-Y., Gotz H., Pauly E., Kolbel S., Egert G.,
Thinnes F.P., Wernet P., Altevogt P., Hilschmann N.;
"Primary structure of class II human histocompatibility antigens. 1st
communication. Amino acid sequence of the N-terminal 198 residues of
the bere chain of a HAA-Pw2,2;PR2,2-alloantigen.";
HODDe-Seyler's Z. Physiol. Chem. 362:1665-1669(1981).
-- MISCELLANBOUS: THE CHAIN SHOWN CONSTITUTED ABOUT 70% OF A POOL OF
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
HLA class II histocompatibility antigen, DW2.2/DR2.2 beta chain
                                                                                       ;
0
                                                         100.0%; Score 26; DB 1; Length 197; 100.0%; Pred. No. 66;
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                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO: 0016020; C: membrane; NAS.
GO; GO: 0016020; C: membrane; NAS.
GO; GO: 0016502; C: membrane; NAS.
GO; GO: 0006955; P: immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR0031597; Ig G1.
InterPro; IPR0031597; Ig G1.
InterPro; IPR0031597; Ig G1.
InterPro; IPR0031597; Ig MHC. II beta.
Pfam; PF00049; MHC. II beta; I.
PFADOM; PD000328; MHC. II beta; I.
SWART; SW00407; IG LIKE; I.
PROSITE; PS50815; IG LIKE; I.
MHC. II.
 FLAVODOXIN-LIKE.
G -> A (IN REF. 1).
7B48C7CCC2B71747 CRC64;
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                                                                                      0; Mismatches
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DOMAIN 1 1 54 EXTRACE
 188 FL
141 G
20714 MW;
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                                                                                      Conservative
                                                                                                                                                                                                              STANDARD;
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3 16
141 1.
197 AA;
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                                                      Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                         48 EKAĞĞ 52
                                                                                                               1 EKAGG 5
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117
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CONFLICT
SEQUENCE
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HUMAN
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                                                                                   Matches
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SEQUENCE FROM N.A.
MEDLINE=95014161; PubMed=7929079;
Turi T.G., Webster P., Rose J.K.;
"Brefeldin A sensitivity and resistance in Schizosaccharomyces pombe.
Isolation of multiple genes conferring resistance.";
J. Biol. Chem. 269:24229-24236(1994).

2

SEQUENCE FROM N.A.

SEQUENCE FROM N.A., AND SEQUENCE OF 36-56.

MEDLINE=93078747; PubMed=1448080;
Toda T., Shimanuki M., Saka Y., Yamano H., Adachi Y.,
Shirakawa M., Kyogoku Y., Yanagida M.;
"Fisakon yeast papl-dependent transcription is negatively regulated by an essential nuclear protein, crml.";
Mol. Cell. Biol. 12:5474-5484(1992).

Schizosaccharomyces pombe (Fission yeast). Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;

Schizosaccharomyces. NCBI\_TaxID=4896;

P25 protein (Brefeldin A resistance profein) OBR1 OR SPAC3C7.14C.

Last sequence update) Last annotation update)

(Rel. 26, Created) (Rel. 26, Last seg

01-JUL-1993 01-JUL-1993 10-OCT-2003

SCHPO

202 AA.

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A MEDLINE=21846401; PubMed=11859360;

RA MODO V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Squorso V., Feat N., Hayles J., Basham D., Bowaman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gonles M., Gonnor R., Cronin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

A Mooney P., Moules S., Mangall K., Murphy L., Niblett D., Odell C.,

RA Noney P., Moules S., Saunders D., Seeger K., Sharp S.,

Ratherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

Rakelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Raylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Hollons M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Borzym K., Langer I., Deck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Goffeau A., Cadieu E., Dreano S., Claure V., Marrst S.M.,

RA Goffeau A., Cadieu E., Dreano S., Calaure V., Marrst S.M.,

RA Goffeau A., Cadieu E., Dreano S., Lelaure V., Garzon A., Thode G.,

Ra Locas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

Ra Dominguez A., Revuelta J.L., Mocreno S., Armstrong J., Forsburg S.L.,

RA Cruttil L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

Ra Shakovski G.V., Ussery D., Barrell B.G., Nurse P.,

Ra Hare 415:871-880 (2002)

Ra Hare 415:871-880 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: UNKNOWN. TARGET OF PAPI TRANSCRIPTION FACTOR. CONFERS BREFELDIN A RESISTANCE IN S.POMBE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBUNIT: Homodimer.
-i- SIMILARITY: Belongs to the wrbA family.
-i- SIMILARITY: Contains 1 flavodoxin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
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Gaps

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0; Indels

0; Mismatches

5; Conservative

Matches

138 EKAĞĞ 142

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RESULT 13 P25\_SCHPO

1 EKAGG 5

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SEQUENCE FROM N.A.
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RNC_LISIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of the Bacillus subtilis genome containing the skin element and many sporulation genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=168 / JH642;
MEDLINE=97124195; PubMed=8969508;
Mizuno M., Masuda S., Takeuchi M.,
Kobayashi Y.;
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE=95658187; PubMed=7968523; Hahn J., Inamine G., Kozlov Y., Dubnau D.A.; "Characterization of comE, a late competence operon of Bacillus subtilis required for the binding and uptake of transforming DNA."; Mol. Microbiol. 10:99-110(1993).
                                                                                                                                                                                                                                                                                                                                                                           ..
0
100.0%; Score 26; DB 1; Length 202; 100.0%; Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
ComE operon protein 1.
COMEA OR COME1 OR BSU25590.
Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
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P39694;
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-!- FUNCTION: Needed for both DNA binding and transport. It is absolutely required for the uptake of transforming DNA but not for binding. Its role in binding may be indirect.
-!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
-!- SUBCELLULAR: TO E.COLI YBAV AND H.INFLUENZAE H11008.
Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
"The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inamine G.S., Dubnau D.; "ComEA, a Bacillus subtilis integral membrane protein required for genetic transformation, is needed for both DNA binding and
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Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
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4E3817FAF982F9DE CRC64;
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DOMAIN 1 CYTOPLASMIC (POTENTIAL).
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28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease III (EC 3.1.26.3) (RNase III).
RNC OR RNCS OR LIN1919.
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EMBL, D84432; BAA12452.1; --
EMBL, Z89117; CAB14501.1; --
PIR, S3963; S39863.
Subtlinst; BG10480; comEA.
InterPro; IPR004509; ComEA.
InterPro; IPR004509; ComEA.
InterPro; IPR004509; HHH.
InterPro; IPR003583; HHH.
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RE STRAIN=CLIP 11262 / Serovar 6a;

RA Glaser P., Frangeul L., Buchiriseser C., Rusniok C., Amend A.,

RA Glaser P., Frangeul L., Buchiriseser C., Rusniok C., Amend A.,

RA Glaser P., Frangeul L., Buchiriseser C., de Darwar A., Dehoux P.,

RA Glaster P., Greche P., Blocack H., Welbrut B., Clarkborty T.,

RA Glaster P., Greche I., Buchiriseser C., de Darwar A., Dehoux P.,

RA Glaster D., Sepin H., Garcia-del Pottillo F. Garrido P., Jackson D.,

RA Glaster D., Raber B., Gomes-Lopez N., Hain T., Bauf J., Jackson D.,

RA Glaster D., Raber B., Gomes-Lopez N., Hain T., Hauf J., Jackson D.,

RA Maticurnan A., Marcy U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

RA Maticurnan S., de Pablos B., Pere-Diaz J.-C., Purcell R.,

RA Memmel B., Rose M., Schlueter T., Simoes N., Terrez A.,

RA Remmel B., Rose M., Schlueter T., Simoes N., Terrez A.,

R. Comparative genomics of Listeria species.", Cosart P.;

R. Comparative genomics of Listeria species.",

R. Comparative genomics of Listeria species.",

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R. SHICKELTIC ACTIVITY: Endomucleolytic Cleavage to 5.-

- FUNCTION: Digest Standard Librarity.

- Instructural R. Locations I DRBM (double-stranded RNA-binding) domain.

- C. C. Tibosomal RNA preductions of some markas (by similarity).

- SHULMKITY: Contains I RNase III domain.

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- SHULM RISSING ACTIVITY: Contains I Rnase III domain.

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- SHULM RNAS: Mossis I Rnase III.

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Search completed: September 18, 2004, 04:26:26 Job time : 4.72549 secs

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h 100.0%; Score 26; DB 1; Length 229; Similarity 100.0%; Pred. No. 77; 5; Conservative 0; Mismatches 0; Indels

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September 18, 2004, 04:00:08; Search time 17.7451 Seconds (without alignments) 88.903 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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	Description	Ogase mis misculu	Ogoxa8 mis miscoli		O82215 chlamydonhi	09zhv2 thiohacillu	Ogandl thiobacillu	OZUSAR SYMPODOCO	OBDAN7 methenogen	OSE115 OFFEE SETE	OBYCY3 calmonella	OBIVER SECTIONS	Ogligo atrentomico	פסלפנסנס	Ollino meanles vii	neas tes	Oll700 measles vir
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O11701 measles vir		sphingomor												O82t50 nvrobacilim				091kn3 castanea sa		neisseria	O9jzm6 neisseria m		07v7d8 prochloroco				07v1t3 prochloroco	
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## ALIGNMENTS

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56 AA.	dn epuer	.11) (F	.a. Worth	a, vero gnathi; 1				tructos				tase act	IEA.	lism, IE					CE14C462	Score 26; DB 11; Pred. No. 1.4e+02; Mismatches 0;
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PRELIMINARY;	Lrel. 13, Lrel. 13,	Liei. 25, Osphatase ENE.	e). : Chordata:			PubMed=112	, Eschrich	or the mou	001).	!T'/5750	51.	F.fructose-bisphosphatase	Finydrolase activity, IEA. Fiphosphoric ester hydrola	P:carbohydrate metabolism; IEA.	5; In FB p	In FB phph		75.1	6162 MW;	100.0%; 100.0%; rative
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JLT 1 (C2 Q9QXC2 Q9QXC2	01-MAY-2000 01-MAY-2000	Fructose-1,6-bisphosphatase FBP1 OR FBPASE 1 GENE.	Mus musculus (Mouse) Eukarvota: Metazoa:	Mammalia; Eutheria; NCBI TaxID=10090;	SEQUENCE FROM N.A.	IISSUE=LIVEI; MEDLINE=21147931; PubMed=11250076;	Stein S., Liehr T., Eschrich K.,	gene.";	Gene 264:215-224(2001)	HSSP; P00636; 1FRP.	MGD; MGI:95492; Fbp1.	GO; GO: 0042132;	GO; GO: 0042578;	GO; GO:0005975;	InterPro: IPR000146; In FB phphtase. Pfam: PF00316; FBPase: 1	ProDom; PD001491; In FB phphtase;	Hydrolase.	NON TER	SEQUENCE	Query Match Best Local Sir Matches 5;
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Chenk R., Chen H., Kim C.J., Meyers M.C., Banh J., Hayashizaki Y.,
Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Ondera C.S.,
Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
Shanidopsis ORF clones."
"Arabidopsis ORF clones."
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"Arabidopsis A.M. Theologis A., Ecker J.R.;
Shmitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, A003748; AAK598441: -.
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Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T., Heidelberg J., Holtzapple B., Khouri H., Federova N.B., Carty H.A. Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O., Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M., Praser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydophila caviae.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
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                                                                                                                                                                             Ecker J.R.;
"Arabidopsis cDNA clones ";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Complete proteome.
SEQUENCE 74 AA; 8743 MW; F5DE70DEE513BBE6 CRC64;
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Pfam; PF02987; LEA; 1.
SROUENCE 68 AA; 7145 MW; 3DAOA82DFA007DC8 CRC64;
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Last sequence update)
Last annotation update)
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EMBL; AE016996; AAP05336.1; -.
TIGR; CCA00594; -.
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01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
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Best Local Similarity
Matches 5; Conserv
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Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
Konning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC F1683 genomic sequence.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21147931; PubMed=11250076;
Stein S., Liehr T., Eschrich K.;
"Characterization of the mouse liver fructose-1,6-bisphosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0042132; F:fructose-bisphosphatase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0042578; F:phosphoric ester hydrolase activity; IEA.
GO; GO:005975; P:carbohydrate metabolism; IEA.
InterPro; IPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 26; DB 11; Length 100.0%; Pred. No. 1.6e+02;
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63 AA; 7074 MW; 19A0AFADDE5682E2 CRC64;
                                                                                                                                                                                                                                                                                                                   Fructose-1,6-bisphosphatase (EC 3.1.3.11) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-077-2000 (TrEMBLrel. 15, Created)
01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
F16B3.11 protein (AT3902480/F16B3_11).
                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                          63 AA
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Gene 264:215-224(2001).
EMBL; AJ245390; CAB65269.1; -.
HSSP; P00636; 1FRP.
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es 5; Conservative
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                                                 EKAGG 5
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Query Match

Best Loc Matches

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Q9M892

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Gaps

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SEQUENCE FROM N.A.

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STRAIN-GOOL / GOI/ ATCC BAA-199 / DSM 3647 / OCM 88;

MEDLINE-22120827; PubMed=12125824;

MARTINEZ-ATIAS R., Henne A., Hartsch T., Merkl R., Schmitz R.A.,

MARTINEZ-ATIAS R., Henne A., Wiezer A., Baeumer S., Jacobi C.,

Martinez-Atias R., Henne A., Wiezer A., Boemecke M., Steckel S.,

Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,

Brutacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,

R. The genome of Methanosarcina mazei: evidence for lateral gene

T. Transfer between Bacteria and Archaea.";

J. Mol. Microbiol. Biotechnol. 4:453-461(2002).

R. Mol. Microbiol. Biotechnol. 4:453-461(2002).

R. Mol. Microbiol. Biotechnol. 4:453-461(2002).

R. GO: GO: GOIGNAD; Firansferase activity; IEA.

GO; GO: GOIGNAD; Firansferase activity; IEA.

R. O; GO: GOIGNAD; Firansferase activity; IEA.

R. O; GO: GOIGNAD; Firansferase activity; IEA.

R. ThterPro; IPROGS83; MTP transferase.

B. Rim: PROG883; MTP transferase.

B. Firm: PROG883; MTP transferase.

B. Firm: PROG883; MTP transferase.
                                                                                                                                                                                                      MEDLINE=22825697; PubMed=12917641;
Palenik B., Brahamsha B., Larimer F.W., Land M., Hauser L., Chain P., Lamerdin J., Regala W., Allen B.E., McCarren J., Paulsen I., Dufresne A., Partensky F., Webb E.A., Waterbury J.;

"The genome of a motile marine Synechococcus.";

Nature 424:1037-1042(2003).

EMBL; BX569693; CAE08098.1; -

SPROUBLIS ARSE Protein; Complete protecome.

SEQUENCE 90 AA; 10321 MW; E60FC6B1902B3D63 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 26; DB 16; Length 90; 100.0%; Pred. No. 2.48+02;
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SEQUENCE 95 AA; 10409 MW; 10D22BFF2445144E CRC64;
                                                                     Symechococcus sp. (strain WH8102).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=84588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methanosarcina mazei (Methanosarcina frisia).
Archaea; Buryarchaeota; Buryarchaeota orders incertae
Methanosarcinales; Methanosarcinaceae; Methanosarcina.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                           Conserved hypothetical
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nes 5, Conserv
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                      SEQUENCE FROM N.A.
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Cannon G.C., Heinhorst S., Soyer F., Shively J.M.;
"The putative carboxysome operon of Thiobacillus denitrificans.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
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Comamonadaceae; Thiomonas.
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NCBI_TaxID=36861;
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Submitted (FBB-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (FBB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AFG46931; AAD02449.1; -.
InterPro; IPR004992; EutN CcmL.
Pfam; PF03319; EutN CcmL; J.
ProDom; PD012510; EUtN CcmL; 1.
SEQUENCE 84 AA; 88779 MW; 4CF8350D591A5C7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR004992; Eutn CcmL.
Pfam; PF03319; Eutn CcmL; 1.
ProDom; PD012510; Eutn CcmL; 1.
SEQUENCE 84 AA; 9110 MW; B975A85088BA838C CRC64;
                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Carboxysome peptide ORF A.
Thiobacillus denitrificans.
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
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                                                                                                                                 84 AA.
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Q7U5V8
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MEDLINE=21534947; PubMed=11677608;
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EMBL, AR003584; BAR73121.1; -.
EMPL, A11951; A11951; AND
Hypothetical protein; Complete
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MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";
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                                                                                                                                                                                                                                                                                     STRAIN-CV. Nipponbare;
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
Overton II. Li., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
Vanaken D.W., Tallon L.J., Koo H., Zismann V., Haiao J., Blunt S.,
Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
Yang Q.Q., Haas B.J., Sub B.B., Peterson J.J., Quackenbush J.,
White O., Salzberg S.L., Fraser C.M.;
Coryza sativa chromosome 3 BAC OSJNBb0021011 genomic sequence.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

Hypothetical protein.
SEQUENCE 118 AA, 12495 MW; D89C1124A459C6C3 CRC64;
                                                                                                                            Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Enterobacteriaceae; Salmonella.
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                  01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
10-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
OSUNBB0021011.17.
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Best Local Similarity 100...
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Berooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., "Complete genome sequence of a multiple drug resistant Salmonella enterica servorar Typhi CT18.";
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
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EMBL, AE016849; AA071922.1; -.

EMBL, AE008908; AAL3246.1.1; -.

EMBL, AL627283; CAD06901.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 120 AA; 12469 MW; 11DF228CDF390A24 CRC64;
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126 AA; 14192 MW; 51EDF6752FE60723 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein SC07383.
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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ilarity 100.0%; Pred. No. 3.3e+02;
Conservative 0; Mismatches 0;
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"Identification of 3 lineages of wild measles virus by the nucleotide sequence analysis of N, P, M, F and L gene for 10 years in Japan."; J. Med. Virol. 52:113-120(1997).

BMBL, D87524; BAA20185.1; ---
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003723; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:000586; F:RNA-directed RNA polymerase activity; IEA.
InterPro; IPR02581; Morbilli_P.
Fiam; PF01647; Morbilli_P.
Fiam; PF01647; Morbilli_P.
Fiam; PF01647; Morbilli_P.
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Paramyxoviridae; Paramyxovirinae; Morbillivirus.
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                               011702;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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MEDLINE=97278133; PubMed=9131467;
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MEDLINE=97278133; PubMed=9131467;
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                                                                                                                                                                                                                                                                         NCBI_TaxID=11234;
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                                                                                                                                                                                   Measles virus
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EMBL, D87540; BAA210201.1; -.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:00033968; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0005390; P:transcription; IEA.
InterPro; IPRO02581; Morbilli.P.
Ffam; PF01647; Morbilli.P.
NON_TER. 128 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL939131; CAB76284.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 126 AA; 13709 MW; 8B36C736317306BD CRC64;
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Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
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01-UUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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MEDLINE=97278133; PubMed=9131467;
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J. Med. Virol. 52:113-120(1997).

EMBL, D87751; BAA20262.1; -.

GO; GO:0003723; F:RNA binding; IEA.

GO; GO:0003723; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:000550; P:transcription; IEA.

InterPro; IPRO2581; Morbilli_P: Pfam; PF01647; Morbilli_P: 1.

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Paramyxoviridae; Paramyxovirinae; Morbillivirus.
NCBI_TaxID=11234;
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                                                01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Sive 0; Mismatches 0;
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